

TABLE 3F					
Genes Corresponding To Differentially Expressed Genes in Figure 13 - Obesity					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1	0.011644	vacuolar protein sorting 28 (yeast) (VPS28), mRNA /cds=(62,727) /gb=NM_016208 /gi=7705884 /ug=Hs.339697 /len=928	NM_016208	Hs.339697	NP_057292
2	0.043827	histone deacetylase 5 (HDAC5), transcript variant 2, mRNA /cds=(305,3418) /gb=NM_139205 /gi=21237798 /ug=Hs.9028 /len=5041	NM_139205	Hs.9028	NP_631944
18	0.026979	histone H1 (0)	X03473		
26	0.025835	nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDT4), mRNA /cds=(191,736) /gb=NM_019094 /gi=24432097 /ug=Hs.355399 /len=3652	NM_019094	Hs.355399	NP_061967
28	0.036211	602184410T1 NIH_MGC_42 cDNA clone IMAGE:4300347 3', mRNA sequence /clone=IMAGE:4300347 /clone_end=3' /gb=BF569051 /gi=11642431 /ug=Hs.352114 /len=1899	BF569051	Hs.352114	
38	0.008631	GPAA1P anchor attachment protein 1 (yeast) (GPAA1), mRNA /cds=(96,1961) /gb=NM_003801 /gi=6031166 /ug=Hs.4742 /len=2047	NM_003801	Hs.4742	NP_003792
64	0.010592	B-cell CLL/lymphoma 7B (BCL7B), transcript variant 1, mRNA /cds=(117,725) /gb=NM_001707 /gi=20336472 /ug=Hs.16269 /len=1690	NM_001707	Hs.16269	NP_619713
78	0.007994	mRNA, expressed in fibroblasts of periodontal ligament, complete cds, clone:PDL-108	AB019409		
101	0.011644	conserved gene amplified in osteosarcoma (OS4), mRNA /cds=(306,1157) /gb=NM_005730 /gi=19923329 /ug=Hs.355816 /len=4833	NM_005730	Hs.355816	NP_005721
103	0.00684	supervillin (SVIL), transcript variant 2, mRNA /cds=(754,7398) /gb=NM_021738 /gi=11496981 /ug=Hs.154567 /len=8300	NM_021738	Hs.154567	NP_068506
105	0.024972	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C) (MEF2C), mRNA /cds=(402,1823) /gb=NM_002397 /gi=19923214 /ug=Hs.78995 /len=4077	NM_002397	Hs.78995	NP_002388

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
106	0.023381	brother of CDO (BOC), mRNA /cds=(133,3477) /gb=NM_033254 /gi=15147239 /ug=Hs.339352 /len=3534	NM_033254	Hs.339352	NP_150279
111	0.046501	casein kinase 2, alpha prime polypeptide (CSNK2A2), mRNA /cds=(164,1216) /gb=NM_001896 /gi=4503096 /ug=Hs.82201 /len=1677	NM_001896	Hs.82201	NP_001887
131	0.014461	AD-012 protein (LOC55833) (=AB040924 KIAA1491)	NM_018449		NP_060919.1
132	0.00922	phosphatidylinositol glycan, class C (PIGC), transcript variant 1, mRNA /cds=(312,1205) /gb=NM_153747 /gi=24430185 /ug=Hs.433030 /len=1514	NM_153747	Hs.433030	NP_714969
148	0.046501	wl84f02.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2431611 3', mRNA sequence /clone=IMAGE:2431611 /clone_end=3' /gb=AI884779 /gi=5589943 /ug=Hs.380770 /len=527	AI884779	Hs.380770	
177	0.049308	G antigen 1	XP_010196		
208	0.008631	ubiquitin-like 3 (UBL3), mRNA /cds=(110,463) /gb=NM_007106 /gi=6005927 /ug=Hs.173091 /len=3323	NM_007106	Hs.173091	NP_009037
210	0.028428	protein tyrosine phosphatase type IVA, member 1 (PTP4A1), mRNA /cds=(650,1171) /gb=NM_003463 /gi=17986281 /ug=Hs.227777 /len=4394	NM_003463	Hs.227777	NP_003454
230	0.024972	staufer, RNA binding protein, 2 (Drosophila) (STAU2), mRNA /cds=(202,1641) /gb=NM_014393 /gi=7657624 /ug=Hs.96870 /len=4058	NM_014393	Hs.96870	NP_055208
247	0.025245	G protein-coupled receptor Edg-2	Y09479		NP_476500
248	0.041279	hemoglobin, beta (HBB), mRNA /cds=(51,494) /gb=NM_000518 /gi=28302128 /ug=Hs.155376 /len=626	NM_000518	Hs.155376	NP_000509
250	8.95E-04	KIAA1243 protein (KIAA1243), mRNA /cds=(388,801) /gb=NM_014048 /gi=7662513 /ug=Hs.151076 /len=1580	NM_014048	Hs.151076	NP_054767
251	7.33E-04	ATPase, Ca transporting, type 2C, member 1 (ATP2C1), mRNA /cds=(236,2995) /gb=NM_014382 /gi=7656909 /ug=Hs.106778 /len=3637	NM_014382	Hs.106778	NP_055197
282	6.62E-04	protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C), mRNA /cds=(58,1011) /gb=NM_005398 /gi=21314622 /ug=Hs.303090 /len=2524	NM_005398	Hs.303090	NP_005389

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
302	0.036549	origin recognition complex, subunit 2-like (yeast) (ORC2L), mRNA /cds=(215,1948) /gb=NM_006190 /gi=21359879 /ug=Hs.41694 /len=2815	NM_006190	Hs.41694	NP_006181
318	0.011644	3'-phosphoadenosine 5'-phosphosulfate synthase 1 (PAPSS1), mRNA /cds=(27,1901) /gb=NM_005443 /gi=20127474 /ug=Hs.3833 /len=2265	NM_005443	Hs.3833	NP_005434
319	2.54E-04	angiopoietin-like 1 (ANGPTL1), mRNA /cds=(434,1909) /gb=NM_004673 /gi=16905518 /ug=Hs.241519 /len=2066	NM_004673	Hs.241519	NP_004664
320	0.013463	hypothetical protein DKFZp564K142 similar to implantation-associated protein (DKFZp564K142), mRNA /cds=(30,1037) /gb=NM_032121 /gi=14149774 /ug=Hs.323562 /len=2241	NM_032121	Hs.323562	NP_115497
356	0.001656	RAB21, member RAS oncogene family (RAB21), mRNA /cds=(256,933) /gb=NM_014999 /gi=7661921 /ug=Hs.184627 /len=2630	NM_014999	Hs.184627	NP_055814
359	0.001915	plakophilin 2=X97675 plakophilin 2b (ORF 38%)	NP_004563		
388	0.017843	MacMarcks	X70326		NP_075385
390	0.009313	UDP-galactose transporter related (UGTREL1), mRNA /cds=(88,1056) /gb=NM_005827 /gi=5032212 /ug=Hs.154073 /len=1186	NM_005827	Hs.154073	NP_005818
393	0.028428	microsomal epoxide hydrolase (EPHX1) gene, complete cds	AF253417		
394	0.014461	FLJ11874 fis, clone HEMBA1007073 /cds=UNKNOWN /gb=AK021936 /gi=10433239 /ug=Hs.367819 /len=2737	AK021936	Hs.367819	
402	0.016648	mRNA for KIAA1250 protein, partial cds. /cds=(140,5473) /gb=AB033076 /gi=14133246 /ug=Hs.9873 /len=7264	AB033076	Hs.9873	
415	0.026653	H4 histone family, member G (H4FG), mRNA /cds=(1,312) /gb=NM_003542 /gi=21071024 /ug=Hs.46423 /len=390	NM_003542	Hs.46423	NP_003533
419	0.041279	SYNCRIP	AB035725		NP_062770
421	0.028428	eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA /cds=(303,3650) /gb=NM_004836 /gi=21361154 /ug=Hs.102506 /len=4662	NM_004836	Hs.102506	NP_004827
423	0.013463	biotinidase (BTD), mRNA /cds=(36,1667) /gb=NM_000060 /gi=4557372 /ug=Hs.78885 /len=2016	NM_000060	Hs.78885	NP_000051

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
455	0.038855	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA /cds=(120,857) /gb=NM_006826 /gi=21464103 /ug=Hs.74405 /len=2166	NM_006826	Hs.74405	NP_006817
462	0.049308	erg protein (ets-related gene)	M21535		NP_004440
533	0.014461	hemoglobin, gamma G (HBG2), mRNA /cds=(54,497) /gb=NM_000184 /gi=28302132 /ug=Hs.386655 /len=583	NM_000184	Hs.386655	NP_000175
563	0.044072	activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4), mRNA /cds=(882,1937) /gb=NM_001675 /gi=4502264 /ug=Hs.181243 /len=2015	NM_001675	Hs.181243	NP_001666
570	0.00987	cycA gene for cyclin A	X68303		
574	0.029213	mRNA for KIAA1274 protein, partial cds. /cds=(265,2850) /gb=AB033100 /gi=20521819 /ug=Hs.300646 /len=4569	AB033100	Hs.300646	
596	0.02722	tubulin, alpha 3 (TUBA3), mRNA /cds=(100,1455) /gb=NM_006009 /gi=17986282 /ug=Hs.433394 /len=1677	NM_006009	Hs.433394	NP_006000
602	0.004871	helicase with zinc finger domain (HELZ), mRNA /cds=(146,5974) /gb=NM_014877 /gi=7661883 /ug=Hs.3085 /len=6274	NM_014877	Hs.3085	NP_055692
608	0.046805	OTF3 gene	Z11900		
638	0.020596	non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), mRNA /cds=(24,794) /gb=NM_145080 /gi=21489972 /ug=Hs.284295 /len=992	NM_145080	Hs.284295	NP_659547
641	0.046805	mRNA for KIAA1119 protein, partial cds. /cds=(1,3783) /gb=AB032945 /gi=6329707 /ug=Hs.172506 /len=7438	AB032945	Hs.172506	
643	0.003746	glucose regulated protein, 58kDa (GRP58), mRNA /cds=(90,1607) /gb=NM_005313 /gi=21361656 /ug=Hs.13751 /len=2074	NM_005313	Hs.13751	NP_005304
673	0.038653	fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), transcript variant 2, mRNA /cds=(507,2642) /gb=NM_022977 /gi=12669908 /ug=Hs.81452 /len=5356	NM_022977	Hs.81452	NP_075266

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
683	0.008631	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin); member 3 (SERPINA3), mRNA /cds=(26,1327) /gb=NM_001085 /gi=9665246 /ug=Hs.234726 /len=1534	NM_001085	Hs.234726	NP_001076
684	0.038855	tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A), mRNA /cds=(282,1649) /gb=NM_001065 /gi=23312372 /ug=Hs.159 /len=2236	NM_001065	Hs.159	NP_001056
689	0.009313	PTK2 protein tyrosine kinase 2 (PTK2), transcript variant 1, mRNA /cds=(231,3389) /gb=NM_153831 /gi=27886591 /ug=Hs.740 /len=4453	NM_153831	Hs.740	NP_722560
690	0.013463	mRNA for KIAA0518 protein, partial cds. /cds=(1,1953) /gb=AB011090 /gi=3043559 /ug=Hs.23763 /len=4617	AB011090	Hs.23763	
692	0.049308	chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1), mRNA /cds=(127,1278) /gb=NM_001276 /gi=4557017 /ug=Hs.75184 /len=1925	NM_001276	Hs.75184	NP_001267
723	0.01911	G protein-coupled receptor kinase 5 (GPRK5), mRNA /cds=(221,1993) /gb=NM_005308 /gi=4885348 /ug=Hs.211569 /len=2557	NM_005308	Hs.211569	NP_005299
727	0.01004	loss of heterozygosity, 11, chromosomal region 2, gene A (LOH11CR2A), mRNA /cds=(1054,2367) /gb=NM_014622 /gi=7657310 /ug=Hs.152944 /len=3380	NM_014622	Hs.152944	NP_055437
730	0.013463	PTD016 protein (LOC51136), mRNA /cds=(183,809) /gb=NM_016125 /gi=21361528 /ug=Hs.30154 /len=1917	NM_016125	Hs.30154	NP_057209
750	0.032277	cDNA FLJ37412 fis, clone BRAMY2028796. /gb=AK094731 /gi=21753846 /ug=Hs.356300 /len=2442	AK094731	Hs.356300	
757	0.036549	603021120F1 NIH_MGC_114 cDNA clone IMAGE:5191733 5', mRNA sequence /clone=IMAGE:5191733 /clone_end=5' /gb=BI488592 /gi=15327820 /ug=Hs.380956 /len=988	BI488592	Hs.380956	
761	0.00326	caldesmon 1 (CALD1), transcript variant 1, mRNA /cds=(230,2611) /gb=NM_033138 /gi=15149460 /ug=Hs.325474 /len=3610	NM_033138	Hs.325474	NP_149347
771	0.001915	zinc finger protein (ZFD25) (62% aa)	AB027251		NP_057304

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
779	0.00632	myosin, heavy polypeptide 9, non-muscle (MYH9), mRNA /cds=(1,5883) /gb=NM_002473 /gi=22507396 /ug=Hs.146550 /len=7274	NM_002473	Hs.146550	NP_002464
780	0.009313	X-box binding protein 1 (XBP1), mRNA /cds=(49,834) /gb=NM_005080 /gi=14110394 /ug=Hs.149923 /len=1836	NM_005080	Hs.149923	NP_005071
786	0.005382	syntaxin 8 (STX8), mRNA /cds=(151,861) /gb=NM_004853 /gi=4759187 /ug=Hs.380938 /len=979	NM_004853	Hs.380938	NP_004844
795	0.023381	procollagen C-endopeptidase enhancer 2 (PCOLCE2), mRNA /cds=(197,1444) /gb=NM_013363 /gi=16904386 /ug=Hs.8944 /len=1988	NM_013363	Hs.8944	NP_037495
796	0.017843	poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525 /len=1362	NM_005016	Hs.63525	NP_114366
797	0.032277	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 1 (cartilage-derived) (CLECSF1), mRNA /cds=(80,673) /gb=NM_005752 /gi=5031636 /ug=Hs.287364 /len=673	NM_005752	Hs.287364	NP_005743
811	0.024972	sterol carrier protein 2 (SCP2), mRNA /cds=(22,1665) /gb=NM_002979 /gi=19923232 /ug=Hs.75760 /len=2572	NM_002979	Hs.75760	NP_002970
815	0.036549	SnRNP assembly defective 1 (SAD1), mRNA /cds=(493,1467) /gb=NM_006590 /gi=5730024 /ug=Hs.12820 /len=2166	NM_006590	Hs.12820	NP_006581
824	0.004961	lipoprotein lipase (LPL), mRNA /cds=(175,1602) /gb=NM_000237 /gi=4557726 /ug=Hs.180878 /len=3549	NM_000237	Hs.180878	NP_000228
833	0.024972	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa (NDUFB3), mRNA /cds=(253,549) /gb=NM_002491 /gi=4505360 /ug=Hs.109760 /len=693	NM_002491	Hs.109760	NP_002482
834	0.01911	tetraspan 3 (TSPAN-3), mRNA /cds=(218,979) /gb=NM_005724 /gi=21264581 /ug=Hs.100090 /len=1842	NM_005724	Hs.100090	NP_005715
837	0.034358	serine/arginine repetitive matrix 2 (SRRM2), mRNA /cds=(226,8484) /gb=NM_016333 /gi=19923465 /ug=Hs.197114 /len=9027	NM_016333	Hs.197114	NP_057417

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
857	0.00632	mitochondrial carrier 1 (MTCH1), nuclear gene encoding mitochondrial protein, mRNA /cds=(1,1119) /gb=NM_014341 /gi=7657344 /ug=Hs.279939 /len=1890	NM_014341	Hs.279939	NP_055156
858	0.011644	calpastatin (CAST), transcript variant 2, mRNA /cds=(155,2215) /gb=NM_173060 /gi=27765084 /ug=Hs.359682 /len=4296	NM_173060	Hs.359682	NP_775085
867	0.016648	insulin-like growth factor binding protein 7 (IGFBP7), mRNA /cds=(23,871) /gb=NM_001553 /gi=4504618 /ug=Hs.119206 /len=1124	NM_001553	Hs.119206	NP_001544
887	0.023381	polyadenylate binding protein-interacting protein 1 (PAIP1), mRNA /cds=(188,1627) /gb=NM_006451 /gi=17511254 /ug=Hs.109643 /len=2764	NM_006451	Hs.109643	NP_006442
890	0.017843	tropomyosin 1 (alpha) (TPM1), mRNA /cds=(151,1005) /gb=NM_000366 /gi=27597084 /ug=Hs.77899 /len=1265	NM_000366	Hs.77899	NP_000357
891	0.00632	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 yeast) (UBE2E3), mRNA /cds=(120,743) /gb=NM_006357 /gi=5454145 /ug=Hs.4890 /len=1294	NM_006357	Hs.4890	NP_006348
892	0.041279	transmembrane 4 superfamily member 6 (TM4SF6), mRNA /cds=(104,841) /gb=NM_003270 /gi=21265115 /ug=Hs.121068 /len=2069	NM_003270	Hs.121068	NP_003261
896	0.005382	hypothetical protein FLJ32949 (FLJ32949), mRNA /cds=(1,2277) /gb=NM_173812 /gi=27883873 /ug=Hs.125472 /len=2277	NM_173812	Hs.125472	NP_776173
899	0.032277	chromosome 21 open reading frame 59 (C21orf59), mRNA /cds=(361,777) /gb=NM_017835 /gi=8923436 /ug=Hs.5811 /len=1245	NM_017835	Hs.5811	NP_067077
900	0.001319	RAB11A, member RAS oncogene family (RAB11A), mRNA /cds=(104,754) /gb=NM_004663 /gi=20149549 /ug=Hs.75618 /len=2474	NM_004663	Hs.75618	NP_004654
903	0.016648	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), mRNA /cds=(112,405) /gb=NM_002966 /gi=4506760 /ug=Hs.400250 /len=649	NM_002966	Hs.400250	NP_002957

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907	0.028428	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) (SFPQ), mRNA /cds=(86,2209) /gb=NM_005066 /gi=4826997 /ug=Hs.180610 /len=3071	NM_005066	Hs.180610	NP_005057
916	0.014461	LIM and senescent cell antigen-like domains 1 (LIMS1) =U09284, PINCH protein	NM_004987		NP_004978
919	0.034358	putative protein tyrosine phosphatase (PTEN) mRNA, complete cds /cds=(1,1212) /gb=U93051 /gi=1916351 /ug=Hs.356062 /len=1212	U93051	Hs.356062	NP_000305
922	0.038855	unc-50 related (DKFZp564G0222), mRNA /cds=(1186,1965) /gb=NM_014044 /gi=24432047 /ug=Hs.13370 /len=2189	NM_014044	Hs.13370	NP_054763
943	0.014461	XIST, coding sequence "a" mRNA (locus DXS399E). /gb=X56199 /gi=37987 /ug=Hs.352403 /len=1614	X56199	Hs.352403	
952	0.00299	mRNA; cDNA DKFZp451O194 (from clone DKFZp451O194) /gb=AL832029 /gi=21732569 /ug=Hs.22559 /len=5226	AL832029	Hs.22559	
963	0.003866	nucleoporin 153kDa (NUP153), mRNA /cds=(201,4628) /gb=NM_005124 /gi=24430145 /ug=Hs.211608 /len=5687	NM_005124	Hs.211608	NP_005115
966	0.01911	CGI-81 protein (DREV1), mRNA /cds=(249,1100) /gb=NM_016025 /gi=19923448 /ug=Hs.279583 /len=3163	NM_016025	Hs.279583	NP_057109
967	0.007397	hepatoma-derived growth factor (high-mobility group protein 1-like) (HDGF), mRNA /cds=(316,1038) /gb=NM_004494 /gi=4758515 /ug=Hs.89525 /len=2376	NM_004494	Hs.89525	NP_004485
972	0.010816	glioma tumor suppressor candidate region gene 2 (GLTSCR2), mRNA /cds=(53,1489) /gb=NM_015710 /gi=21359905 /ug=Hs.421907 /len=1610	NM_015710	Hs.421907	NP_056525
974	0.046501	putative Rab5 GDP/GTP exchange factor (RABEX5), mRNA /cds=(78,1553) /gb=NM_014504 /gi=7657495 /ug=Hs.187660 /len=3740	NM_014504	Hs.187660	NP_055319
1001	4.86E-04	RAD23 B (S. cerevisiae) (RAD23B), mRNA /cds=(352,1581) /gb=NM_002874 /gi=19924138 /ug=Hs.404283 /len=2943	NM_002874	Hs.404283	NP_002865
1055	0.030302	U50' snoRNA and U50 snoRNA	AB017710		



Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1090	0.00274	protein phosphatase methylesterase-1 (PME-1), mRNA /cds=(100,1260) /gb=NM_016147 /gi=7706644 /ug=Hs.63304 /len=2484	NM_016147	Hs.63304	NP_057231
1117	0.044748	CDK5 regulatory subunit associated protein 3 (CDK5RAP3), mRNA /cds=(994,2253) /gb=NM_025197 /gi=13376787 /ug=Hs.20157 /len=2538	NM_025197	Hs.20157	NP_788276
1181	0.023381	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa (NDUFC2), mRNA /cds=(151,510) /gb=NM_004549 /gi=19923255 /ug=Hs.193313 /len=2168	NM_004549	Hs.193313	NP_004540
1184	0.007397	mannosidase, alpha, class 1A, member 2 (MAN1A2), mRNA /cds=(521,2446) /gb=NM_006699 /gi=5729912 /ug=Hs.367638 /len=2792	NM_006699	Hs.367638	NP_006690
1193	0.038855	CGI-100 protein (CGI-100), mRNA /cds=(113,802) /gb=NM_016040 /gi=19923441 /ug=Hs.348996 /len=3635	NM_016040	Hs.348996	NP_057124
1194	0.016648	proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA /cds=(86,811) /gb=NM_002790 /gi=23110941 /ug=Hs.76913 /len=1023	NM_002790	Hs.76913	NP_002781
1206	0.043827	ATP synthase, H transporting, mitochondrial F1 complex, gamma polypeptide 1 (ATP5C1), mRNA /cds=(32,925) /gb=NM_005174 /gi=4885078 /ug=Hs.155433 /len=1078	NM_005174	Hs.155433	NP_005165
1209	0.016648	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) (MPP6), mRNA /cds=(300,1922) /gb=NM_016447 /gi=21361597 /ug=Hs.108931 /len=2201	NM_016447	Hs.108931	NP_057531
1223	0.009313	KIAA0874	AB020681		NP_056023
1228	0.007994	cDNA FLJ14076 fis, clone HEMBB1001925. /gb=AK024138 /gi=10436445 /ug=Hs.406835 /len=2124	AK024138	Hs.406835	
1235	0.016648	mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026) /gb=AL050367 /gi=4914600 /ug=Hs.66762 /len=3958	AL050367	Hs.66762	
1237	0.049308	similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA /cds=(67,558) /gb=NM_022731 /gi=12232386 /ug=Hs.118064 /len=1811	NM_022731	Hs.118064	NP_073568

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1250	0.030302	nuclear protein, ataxia-telangiectasia locus (NPAT), mRNA /cds=(35,4318) /gb=NM_002519 /gi=4505430 /ug=Hs.89385 /len=5895	NM_002519	Hs.89385	NP_002510
1285	0.003866	butyrophilin, subfamily 3, member A1 (BTN3A1), mRNA /cds=(360,1901) /gb=NM_007048 /gi=19923378 /ug=Hs.284283 /len=3452	NM_007048	Hs.284283	NP_008979
1292	0.026653	cellular retinoic acid binding protein 1 (CRABP1), mRNA /cds=(75,488) /gb=NM_004378 /gi=4758051 /ug=Hs.346950 /len=735	NM_004378	Hs.346950	NP_004369
1335	0.042116	hypothetical protein MGC11316 (MGC11316), mRNA /cds=(116,226) /gb=NM_032932 /gi=14249729 /ug=Hs.7985 /len=781	NM_032932	Hs.7985	NP_116321
1336	0.020453	Novel mRNA from chromosome 1, which has similarities to BAT2 genes /cds=(58,8163) /gb=AL096857 /gi=5541862 /ug=Hs.69559 /len=10174	AL096857	Hs.69559	NP_055987
1363	0.047541	nucleoporin Nup43 (Nup43), mRNA /cds=(646,1176) /gb=NM_024647 /gi=21362033 /ug=Hs.53263 /len=3118	NM_024647	Hs.53263	NP_078923
1375	0.023381	similar to embryonic seven-span transmembrane protein-like protein (H. sapiens) (LOC135428), mRNA	XM_059770		
1406	0.020453	fibrillin 1 (Marfan syndrome) (FBN1), mRNA /cds=(134,8749) /gb=NM_000138 /gi=24430140 /ug=Hs.750 /len=9749	NM_000138	Hs.750	NP_000129
1424	0.034358	RAP1A, member of RAS oncogene family (RAP1A), mRNA /cds=(313,867) /gb=NM_002884 /gi=4506412 /ug=Hs.865 /len=1579	NM_002884	Hs.865	NP_002875
1426	0.020453	chemokine (C-C motif) ligand 13 (CCL13), mRNA /cds=(76,372) /gb=NM_005408 /gi=22538799 /ug=Hs.11383 /len=861	NM_005408	Hs.11383	NP_005399
1441	0.034358	RE1-silencing transCRiption factor (REST)	NM_005612		NP_005603
1442	0.041279	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3), mRNA /cds=(382,3126) /gb=NM_015049 /gi=13027379 /ug=Hs.154248 /len=6470	NM_015049	Hs.154248	NP_055864

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1443	0.004569	cDNA FLJ13106 fis, clone NT2RP3002455, highly similar to mRNA for KIAA0678 protein. /gb=AK023168 /gi=10434970 /ug=Hs.12707 /len=3985	AK023168	Hs.12707	
1444	3.17E-04	cDNA: FLJ23165 fis, clone LNG09846. /gb=AK026818 /gi=10439763 /ug=Hs.279898 /len=2117	AK026818	Hs.279898	
1451	0.049308	polymerase (RNA) II (DNA directed) polypeptide G (POLR2G), mRNA /cds=(107,625) /gb=NM_002696 /gi=4505946 /ug=Hs.14839 /len=828	NM_002696	Hs.14839	NP_002687
1453	0.01004	methyl-CpG binding domain protein 2 (MBD2), transcript variant testis-specific, mRNA /cds=(230,1138) /gb=NM_015832 /gi=21464120 /ug=Hs.25674 /len=2792	NM_015832	Hs.25674	NP_056647
1454	0.041279	Dmx-like 1 (DMXL1), mRNA /cds=(81,9164) /gb=NM_005509 /gi=21536473 /ug=Hs.181042 /len=11072	NM_005509	Hs.181042	NP_005500
1456	0.009313	CGI-74 protein (CGI-59), mRNA /cds=(1,1209) /gb=NM_016019 /gi=7706309 /ug=Hs.7194 /len=2296	NM_016019	Hs.7194	NP_057103
1473	0.01004	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) (HSPA5), mRNA /cds=(205,2169) /gb=NM_005347 /gi=21361242 /ug=Hs.75410 /len=3925	NM_005347	Hs.75410	NP_005338
1485	0.016648	SRY (sex determining region Y)-box 5 (SOX5), transcript variant B, mRNA /cds=(373,2625) /gb=NM_152989 /gi=23308714 /ug=Hs.87224 /len=4492	NM_152989	Hs.87224	NP_821078
1492	0.041279	pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, mRNA /cds=(2242,3633) /gb=NM_006718 /gi=27894292 /ug=Hs.75825 /len=4816	NM_006718	Hs.75825	NP_006709
1497	0.012483	hypothetical protein MGC45474 (MGC45474), mRNA /cds=(218,2035) /gb=NM_152369 /gi=22748794 /ug=Hs.234101 /len=2384	NM_152369	Hs.234101	
1507	0.048643	ribosomal protein S27-like (RPS27L), mRNA /cds=(73,327) /gb=NM_015920 /gi=18490988 /ug=Hs.108957 /len=523	NM_015920	Hs.108957	NP_057004
1515	0.026653	ATPase, H transporting, lysosomal 70kDa, V1 subunit A, isoform 1 (ATP6V1A1), mRNA /cds=(67,1920) /gb=NM_001690 /gi=19913423 /ug=Hs.281866 /len=4567	NM_001690	Hs.281866	NP_001681

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1526	0.01004	similar to rat myomegalin (LOC64182), mRNA /cds=(336,1268) /gb=NM_022359 /gi=21314705 /ug=Hs.333512 /len=1717	NM_022359	Hs.333512	NP_071754
1528	0.017843	tubulin, alpha, ubiquitous (K-ALPHA-1), mRNA /cds=(68,1423) /gb=NM_006082 /gi=5174476 /ug=Hs.334842 /len=1596	NM_006082	Hs.334842	NP_006073
1540	0.005835	ribosomal protein S4, X-linked (RPS4X), mRNA /cds=(36,827) /gb=NM_001007 /gi=17981705 /ug=Hs.389933 /len=916	NM_001007	Hs.389933	NP_000998
1550	0.004961	proteasome (prosome, macropain) subunit, alpha type, 3 (PSMA3), transcript variant 1, mRNA /cds=(47,814) /gb=NM_002788 /gi=23110937 /ug=Hs.346918 /len=949	NM_002788	Hs.346918	NP_687033
1551	0.01004	insulin induced gene 1 (INSIG1)	NM_005542		NP_005533
1557	0.020453	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530	BF814502	Hs.446594	
1558	0.003552	signal-induced proliferation-associated 1 like 1 (KIAA0440), mRNA /cds=(349,5763) /gb=NM_015556 /gi=7662125 /ug=Hs.172180 /len=6028	NM_015556	Hs.172180	NP_056371
1559	0.026653	stromal cell derived factor receptor 1 (SDFR1), transcript variant beta, mRNA /cds=(139,1335) /gb=NM_012428 /gi=6912645 /ug=Hs.389371 /len=2388	NM_012428	Hs.389371	NP_059429
1561	0.001592	translocating chain-associating membrane protein (TRAM), mRNA /cds=(92,1216) /gb=NM_014294 /gi=19923404 /ug=Hs.4147 /len=2722	NM_014294	Hs.4147	NP_055109
1562	0.01004	casein kinase 2, alpha 1 polypeptide (CSNK2A1), mRNA /cds=(149,1324) /gb=NM_001895 /gi=4503094 /ug=Hs.155140 /len=2195	NM_001895	Hs.155140	NP_808228
1567	0.041279	RAD21 (S. pombe) (RAD21), mRNA /cds=(185,2080) /gb=NM_006265 /gi=5453993 /ug=Hs.81848 /len=3647	NM_006265	Hs.81848	NP_006256
1569	0.001199	inositol polyphosphate-5-phosphatase, 72kDa (INPP5E), mRNA /cds=(6,1583) /gb=NM_015160 /gi=24308012 /ug=Hs.75353 /len=2097	NM_015160	Hs.75353	NP_055975
1573	0.015521	fibromodulin (FMOD), mRNA /cds=(21,1151) /gb=NM_002023 /gi=5016093 /ug=Hs.230 /len=2863	NM_002023	Hs.230	NP_002014

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1581	0.023381	SH3 domain binding glutamic acid-rich protein like 3 (SH3BGR13), mRNA /cds=(72,353) /gb=NM_031286 /gi=13775197 /ug=Hs.109051 /len=764	NM_031286	Hs.109051	NP_112576
1585	0.036549	retinal outer segment membrane protein 1 (ROM1), mRNA /cds=(132,1187) /gb=NM_000327 /gi=19743809 /ug=Hs.281564 /len=1477	NM_000327	Hs.281564	NP_000318
1588	0.012525	cDNA FLJ30869 fis, clone FEBRA2004224. /gb=AK055431 /gi=16550154 /ug=Hs.349611 /len=2423	AK055431	Hs.349611	
1589	0.030302	signal sequence receptor, delta (translocon-associated protein delta) (SSR4), mRNA /cds=(50,571) /gb=NM_006280 /gi=5454089 /ug=Hs.102135 /len=642	NM_006280	Hs.102135	NP_006271
1599	0.017843	protein XP_037672 (aa, 58%)	XP_037672		
1640	6.62E-04	binder of Arl Two (BART1), mRNA /cds=(115,606) /gb=NM_012106 /gi=17978472 /ug=Hs.9552 /len=1973	NM_012106	Hs.9552	NP_036238
1661	0.014461	cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa (CRSP3), mRNA /cds=(120,4226) /gb=NM_004830 /gi=7019352 /ug=Hs.29679 /len=5176	NM_004830	Hs.29679	NP_057063
1664	0.007994	nq11c09.s1 NCI_CGAP_Thy1 cDNA clone IMAGE:1143568 similar to gb:A18658 INSULIN RECEPTOR PRECURSOR mRNA sequence /clone=IMAGE:1143568 /gb=AA627170 /gi=2540214 /ug=Hs.404836 /len=408	AA627170	Hs.404836	
1702	0.005259	prostatic binding protein (PBP), mRNA /cds=(111,674) /gb=NM_002567 /gi=4505620 /ug=Hs.80423 /len=1444	NM_002567	Hs.80423	NP_002558
1720	0.046501	KIAA0971 protein (KIAA0971), mRNA /cds=(59,2005) /gb=NM_014929 /gi=7662421 /ug=Hs.84429 /len=4999	NM_014929	Hs.84429	NP_055744
1733	0.013463	cDNA FLJ30649 fis, clone CTONG2006562. /gb=AK055211 /gi=16549888 /ug=Hs.167700 /len=3061	AK055211	Hs.167700	
1763	0.043827	zinc finger protein 36, C3H type-like 1 (ZFP36L1), mRNA /cds=(131,1147) /gb=NM_004926 /gi=15812179 /ug=Hs.85155 /len=3022	NM_004926	Hs.85155	NP_004917

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1770	0.00326	actin, gamma 1 (ACTG1), mRNA /cds=(75,1202) /gb=NM_001614 /gi=11038618 /ug=Hs.14376 /len=1919	NM_001614	Hs.14376	NP_001605
1771	0.034358	melanoma antigen, family D, 2 (MAGED2), mRNA /cds=(97,1917) /gb=NM_014599 /gi=21264316 /ug=Hs.4943 /len=2077	NM_014599	Hs.4943	NP_803182
1780	0.046501	cDNA FLJ11997 fis, clone HEMBB1001458. /gb=AK022059 /gi=10433379 /ug=Hs.432755 /len=2393	AK022059	Hs.432755	
1789	0.017843	KIAA1185 protein (KIAA1185), mRNA /cds=(29,1780) /gb=NM_020710 /gi=24308206 /ug=Hs.268488 /len=2693	NM_020710	Hs.268488	NP_065761
1798	0.004205	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa (NDUFV1), mRNA /cds=(70,1464) /gb=NM_007103 /gi=20149567 /ug=Hs.7744 /len=1566	NM_007103	Hs.7744	NP_009034
1799	0.023381	hypothetical protein MGC10911 (MGC10911), mRNA /cds=(234,602) /gb=NM_032302 /gi=14150059 /ug=Hs.85573 /len=985	NM_032302	Hs.85573	NP_115678
1810	0.046501	hypothetical protein FLJ12716 (FLJ12716), mRNA /cds=(66,2513) /gb=NM_021942 /gi=21361577 /ug=Hs.5354 /len=3522	NM_021942	Hs.5354	NP_068761
1836	0.014461	hypothetical protein FLJ23445 (FLJ23445), mRNA /cds=(44,658) /gb=NM_025075 /gi=13376622 /ug=Hs.288151 /len=963	NM_025075	Hs.288151	NP_079351
1840	0.043827	alphoid repetitive DNA, subclone pHS53	M28031		
1842	0.043827	Kruppel-like factor 5 (intestinal) (KLF5), mRNA /cds=(312,1685) /gb=NM_001730 /gi=14251214 /ug=Hs.84728 /len=3359	NM_001730	Hs.84728	NP_001721
1847	3.93E-04	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_153649	Hs.85844	NP_705935
1860	0.036549	hypothetical protein FLJ20559 (FLJ20559), mRNA /cds=(211,810) /gb=NM_017881 /gi=8923529 /ug=Hs.98135 /len=1172	NM_017881	Hs.98135	NP_060351
1879	0.011644	Rab9 effector p40 (RAB9P40), mRNA /cds=(150,1268) /gb=NM_005833 /gi=5032014 /ug=Hs.19012 /len=1297	NM_005833	Hs.19012	NP_005824

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1880	0.016648	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), mRNA /cds=(75,746) /gb=NM_004181 /gi=21361090 /ug=Hs.76118 /len=1119	NM_004181	Hs.76118	NP_004172
1932	0.034358	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 (SMARCD2), mRNA /cds=(423,1850) /gb=NM_003077 /gi=21264350 /ug=Hs.250581 /len=2704	NM_003077	Hs.250581	NP_003068
1947	0.041279	transforming, acidic coiled-coil containing protein 1 (TACC1), mRNA /cds=(321,2738) /gb=NM_006283 /gi=5454099 /ug=Hs.173159 /len=7758	NM_006283	Hs.173159	NP_006274
1952	0.007397	target of myb1 (chicken) (TOM1), mRNA /cds=(62,1540) /gb=NM_005488 /gi=4885636 /ug=Hs.9482 /len=2310	NM_005488	Hs.9482	NP_005479
1972	0.009313	mitochondrion, complete genome	NC_001807		
1981	0.004961	SKB1 (S. pombe) (SKB1), mRNA /cds=(92,2005) /gb=NM_006109 /gi=20070219 /ug=Hs.12912 /len=2413	NM_006109	Hs.12912	NP_006100
1991	0.049308	inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA /cds=(93,2369) /gb=NM_006839 /gi=5803114 /ug=Hs.78504 /len=2697	NM_006839	Hs.78504	NP_006830
2003	0.046501	serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 2 (SERPINH2), mRNA /cds=(88,1344) /gb=NM_001235 /gi=4502596 /ug=Hs.9930 /len=2047	NM_001235	Hs.9930	
2006	0.038855	clathrin, light polypeptide (Lcb) (CLTB), transcript variant brain, mRNA /cds=(173,862) /gb=NM_007097 /gi=6005994 /ug=Hs.380749 /len=1134	NM_007097	Hs.380749	NP_009028
2016	0.014461	HSPC049 protein (HSPC049), mRNA /cds=(8,2233) /gb=NM_014149 /gi=7661753 /ug=Hs.172622 /len=2610	NM_014149	Hs.172622	NP_054868
2039	0.016648	phosphatidyl inositol glycan class T (PIGT), mRNA /cds=(20,1756) /gb=NM_015937 /gi=23397652 /ug=Hs.84038 /len=2171	NM_015937	Hs.84038	NP_057021
2045	0.036549	T-cell activation protein (PGR1), mRNA /cds=(146,529) /gb=NM_033296 /gi=15193293 /ug=Hs.406590 /len=1534	NM_033296	Hs.406590	NP_150638
2046	0.005382	legumain (LGMN), mRNA /cds=(142,1443) /gb=NM_005606 /gi=21914880 /ug=Hs.18069 /len=1981	NM_005606	Hs.18069	NP_005597

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2073	0.032277	transcription factor B1, mitochondrial (TFB1M), mRNA /cds=(73,1113) /gb=NM_016020 /gi=7705784 /ug=Hs.279908 /len=1290	NM_016020	Hs.279908	NP_057104
2100	0.041279	complement component 1, q subcomponent binding protein (C1QBP), nuclear gene encoding mitochondrial protein, mRNA /cds=(79,927) /gb=NM_001212 /gi=11038669 /ug=Hs.78614 /len=1332	NM_001212	Hs.78614	NP_001203
2141	0.024972	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), mRNA /cds=(214,2262) /gb=NM_003205 /gi=4585865 /ug=Hs.21704 /len=4202	NM_003205	Hs.21704	NP_003196
2155	0.030302	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
2179	0.017843	nuclear antigen Sp100 (SP100), mRNA /cds=(32,2671) /gb=NM_003113 /gi=19923235 /ug=Hs.77617 /len=3579	NM_003113	Hs.77617	NP_003104
2190	0.049308	Deleted in split-hand/split-foot 1 region (DSS1), mRNA /cds=(129,341) /gb=NM_006304 /gi=5453639 /ug=Hs.333495 /len=509	NM_006304	Hs.333495	NP_006295
2205	0.024972	apoptosis-related protein TFAR15 (TFAR15)	AF022385		NP_665859
2212	0.001089	chromosome 21 open reading frame 4 (C21orf4), mRNA /cds=(159,635) /gb=NM_006134 /gi=8659558 /ug=Hs.284142 /len=750	NM_006134	Hs.284142	NP_006125
2214	0.001915	ts79a05.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2237456 3', mRNA sequence /clone=IMAGE:2237456 /clone_end=3' /gb=AI917390 /gi=5637245 /ug=Hs.99415 /len=462	AI917390	Hs.99415	
2230	0.00684	PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1), mRNA /cds=(81,2879) /gb=NM_000534 /gi=11496979 /ug=Hs.111749 /len=3121	NM_000534	Hs.111749	NP_000525
2235	0.036549	tight junction protein 2 (zona occludens 2) (TJP2), mRNA /cds=(80,3430) /gb=NM_004817 /gi=4759341 /ug=Hs.75608 /len=4484	NM_004817	Hs.75608	NP_004808
2253	0.021876	small EDRK-rich factor 2 (SERF2), mRNA /cds=(1023,1319) /gb=NM_005770 /gi=21361286 /ug=Hs.380718 /len=1408	NM_005770	Hs.380718	NP_005761



Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2255	0.023381	cadherin 5, type 2, VE-cadherin (vascular epithelium) (CDH5), mRNA /cds=(121,2475) /gb=NM_001795 /gi=14589894 /ug=Hs.76206 /len=4098	NM_001795	Hs.76206	NP_001786
2256	0.028428	splicing factor 3a, subunit 3, 60kDa (SF3A3), mRNA /cds=(9,1514) /gb=NM_006802 /gi=5803166 /ug=Hs.77897 /len=2733	NM_006802	Hs.77897	NP_006793
2264	0.021876	genomic protocadherin gamma cluster (PCDHG@) on chromosome 5	NG_000012		
2271	0.036549	transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>	AF196779		
2273	0.005835	Pirin (PIR), mRNA /cds=(231,1103) /gb=NM_003662 /gi=4505822 /ug=Hs.424966 /len=1318	NM_003662	Hs.424966	NP_003653
2285	0.011644	cDNA FLJ40438 fis, clone TEST12039776, highly similar to POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IIB (EC 3.6.1.-). /gb=AK097757 /gi=21757625 /ug=Hs.429537 /len=1923	AK097757	Hs.429537	
2296	0.01004	serine/threonine kinase 38 like (STK38L), mRNA /cds=(174,1568) /gb=NM_015000 /gi=24307970 /ug=Hs.184523 /len=4725	NM_015000	Hs.184523	NP_055815
2304	0.028428	hypothetical gene supported by AK026099 (LOC128680), mRNA	XM_072157		
2314	0.023381	specificity protein 3 (SP3) mRNA, complete cds /cds=(385,2526) /gb=AY070137 /gi=18091786 /ug=Hs.154295 /len=3979	AY070137	Hs.154295	
2340	0.046501	mRNA; cDNA DKFZp434F2311 (from clone DKFZp434F2311) /gb=AL137603 /gi=6808349 /ug=Hs.233890 /len=842	AL137603	Hs.233890	
2395	0.038855	Purkinje cell protein 4 (PCP4), mRNA /cds=(59,247) /gb=NM_006198 /gi=5453857 /ug=Hs.80296 /len=540	NM_006198	Hs.80296	NP_006189
2396	0.004569	nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds. /cds=(80,6007) /gb=M69181 /gi=641957 /ug=Hs.296842 /len=7596	M69181	Hs.296842	
2399	0.030302	mitochondrion, complete genome	NC_001807		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2434	0.016648	small nuclear ribonucleoprotein D3 polypeptide 18kDa (SNRPD3), mRNA /cds=(88,468) /gb=NM_004175 /gi=4759159 /ug=Hs.1575 /len=626	NM_004175	Hs.1575	NP_004166
2466	0.01911	likely ortholog of mouse gene trap locus 3 (GTL3), mRNA /cds=(257,838) /gb=NM_013242 /gi=8392874 /ug=Hs.279818 /len=1278	NM_013242	Hs.279818	NP_037374
2477	0.030302	of human GTP-binding protein G25K	AL121737		NP_426359
2497	0.023381	YEA4 protein (YEA), mRNA /cds=(301,1296) /gb=NM_032826 /gi=21314760 /ug=Hs.292566 /len=2334	NM_032826	Hs.292566	NP_116215
2506	0.001199	bHLH-PAS transcription factor MOP9 (MOP9) mRNA, long form, complete cds, alternatively spliced /cds=(58,1815) /gb=AF231338 /gi=7963663 /ug=Hs.222024 /len=2008	AF231338	Hs.222024	NP_064568
2525	0.016648	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
2534	0.020453	dendritic cell protein (GA17), mRNA /cds=(53,1177) /gb=NM_006360 /gi=23397428 /ug=Hs.406648 /len=1268	NM_006360	Hs.406648	NP_006351
2545	0.028428	chromosome 8 open reading frame 1 (C8orf1), mRNA /cds=(346,1863) /gb=NM_004337 /gi=4757889 /ug=Hs.40539 /len=4199	NM_004337	Hs.40539	NP_004328
2564	0.034358	mitochondrion, complete genome	NC_001807		
2588	0.049308	apolipoprotein D (APOD), mRNA /cds=(62,631) /gb=NM_001647 /gi=4502162 /ug=Hs.75736 /len=809	NM_001647	Hs.75736	NP_001638
2616	0.012525	baculoviral IAP repeat-containing 6 (apollon) (BIRC6), mRNA /cds=(1,14490) /gb=NM_016252 /gi=10442821 /ug=Hs.250646 /len=14490	NM_016252	Hs.250646	NP_057336
2649	0.023381	zizimin1 (zizimin1), mRNA /cds=(56,6265) /gb=NM_015296 /gi=24308028 /ug=Hs.8021 /len=7522	NM_015296	Hs.8021	NP_056111
2666	0.00274	yeast Sec31p (KIAA0905), mRNA /cds=(54,3716) /gb=NM_014933 /gi=7662369 /ug=Hs.70266 /len=4129	NM_014933	Hs.70266	NP_057295

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2680	0.003866	SEC63, endoplasmic reticulum translocon component (S. cerevisiae (SEC63L), mRNA /cds=(133,2415) /gb=NM_007214 /gi=14591934 /ug=Hs.31575 /len=3368	NM_007214	Hs.31575	NP_009145
2698	0.008631	topoisomerase (DNA) II alpha 170kDa (TOP2A), mRNA /cds=(127,4722) /gb=NM_001067 /gi=19913405 /ug=Hs.156346 /len=5698	NM_001067	Hs.156346	NP_001058
2716	0.021876	general transcription factor IIIC, polypeptide 3, 102kDa (GTF3C3), mRNA /cds=(94,2754) /gb=NM_012086 /gi=6912397 /ug=Hs.90847 /len=2961	NM_012086	Hs.90847	NP_036218
2718	0.016648	17-beta-hydroxysteroid dehydrogenase type VII isoform mRNA, complete cds. /cds=(79,414) /gb=AF165514 /gi=9294734 /ug=Hs.380900 /len=1272	AF165514	Hs.380900	NP_057455
2720	0.002294	mitogen-activated protein kinase kinase kinase 5 (MAP4K5), mRNA /cds=(321,2861) /gb=NM_006575 /gi=14589908 /ug=Hs.246970 /len=3000	NM_006575	Hs.246970	NP_006566
2730	0.007994	small membrane protein 1 (SMP1), mRNA /cds=(151,624) /gb=NM_014313 /gi=20357549 /ug=Hs.107979 /len=2284	NM_014313	Hs.107979	NP_055128
2732	0.016648	Similar to RIKEN cDNA 4921510P06 gene, clone MGC:9752 IMAGE:3855177, mRNA, complete cds	BC009053		NP_055494
2741	0.00632	golgi SNAP receptor complex member 1 (GOSR1), mRNA /cds=(13,765) /gb=NM_004871 /gi=4758455 /ug=Hs.8868 /len=999	NM_004871	Hs.8868	NP_004862
2743	0.021876	clone MGC:9947 IMAGE:3876105, mRNA, complete cds /cds=(51,2216) /gb=BC013590 /gi=15488925 /ug=Hs.2437 /len=2651	BC013590	Hs.2437	
2773	0.034358	nucleosome assembly protein 1-like 1 (NAP1L1), transcript variant 1, mRNA /cds=(125,1300) /gb=NM_139207 /gi=21327707 /ug=Hs.302649 /len=3582	NM_139207	Hs.302649	NP_631946
2779	0.001747	nuclear factor (erythroid-derived 2)-like 2 (NFE2L2), mRNA /cds=(114,1931) /gb=NM_006164 /gi=20149575 /ug=Hs.155396 /len=2439	NM_006164	Hs.155396	NP_006155

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2791	0.034358	hypothetical protein FLJ10283 (FLJ10283), mRNA /cds=(218,1039) /gb=NM_018046 /gi=8922325 /ug=Hs.284216 /len=1876	NM_018046	Hs.284216	NP_060516
2811	0.003552	DnaJ (Hsp40) subfamily C, member 3 (DNAJC3), mRNA /cds=(28,1542) /gb=NM_006260 /gi=24234721 /ug=Hs.9683 /len=1542	NM_006260	Hs.9683	NP_006251
2829	8.95E-04	mitochondrion, complete genome	NC_001807		
2851	0.021876	allograft inflammatory factor 1 (AIF1), transcript variant 2, mRNA /cds=(454,852) /gb=NM_004847 /gi=6680470 /ug=Hs.76364 /len=1363	NM_004847	Hs.76364	NP_116573
2865	0.023381	nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDT4), mRNA /cds=(191,736) /gb=NM_019094 /gi=24432097 /ug=Hs.355399 /len=3652	NM_019094	Hs.355399	NP_061967
2892	0.01004	t-complex 1 (TCP1), mRNA /cds=(22,1692) /gb=NM_030752 /gi=13540472 /ug=Hs.4112 /len=2019	NM_030752	Hs.4112	NP_110379
2964	0.023381	ADP-ribosylation factor domain protein 1, 64kDa (ARFD1), transcript variant alpha, mRNA /cds=(23,1747) /gb=NM_001656 /gi=15208639 /ug=Hs.792 /len=3565	NM_001656	Hs.792	NP_150231
3000	0.043827	clone IMAGE:5590200, mRNA /gb=BC035781 /gi=23272860 /ug=Hs.12862 /len=2951	BC035781	Hs.12862	
3008	0.012525	nuclear receptor subfamily 2, group F, member 2 (NR2F2), mRNA /cds=(343,1587) /gb=NM_021005 /gi=14149745 /ug=Hs.347991 /len=1740	NM_021005	Hs.347991	NP_066285
3009	0.043827	Hypothetical protein(cDNA: FLJ23391 fis, clone HEP17320)	AK027044		NP_006708
3015	0.00299	mitochondrion, complete genome	NC_001807		
3046	0.017843	kinesin family member 3B (KIF3B), mRNA /cds=(168,2411) /gb=NM_004798 /gi=4758645 /ug=Hs.301206 /len=4724	NM_004798	Hs.301206	NP_004789
3051	0.010816	clone MGC:45564 IMAGE:4384472, mRNA, complete cds /cds=(188,1123) /gb=BC036746 /gi=22477830 /ug=Hs.132230 /len=3767	BC036746	Hs.132230	
3073	0.043827	KIAA0174 gene product (KIAA0174), mRNA /cds=(64,1158) /gb=NM_014761 /gi=7661971 /ug=Hs.75824 /len=2348	NM_014761	Hs.75824	NP_055576

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3081	0.049308	transmembrane 4 superfamily member 6 (TM4SF6), mRNA /cds=(104,841) /gb=NM_003270 /gi=21265115 /ug=Hs.121068 /len=2069	NM_003270	Hs.121068	NP_003261
3084	0.028811	nucleobindin 2 (NUCB2), mRNA /cds=(220,1482) /gb=NM_005013 /gi=4826869 /ug=Hs.3164 /len=1586	NM_005013	Hs.3164	NP_005004
3093	0.041279	cDNA FLJ38472 fis, clone FEBRA2022148. /gb=AK095791 /gi=21755125 /ug=Hs.50150 /len=2454	AK095791	Hs.50150	
3170	0.017843	chromosome 20 open reading frame 64 (C20orf64), mRNA /cds=(246,1007) /gb=NM_033550 /gi=19923655 /ug=Hs.282990 /len=2207	NM_033550	Hs.282990	NP_291028
3171	0.041279	transforming, acidic coiled-coil containing protein 1 (TACC1), mRNA /cds=(321,2738) /gb=NM_006283 /gi=5454099 /ug=Hs.173159 /len=7758	NM_006283	Hs.173159	NP_006274
3189	0.026653	melanoma adhesion molecule (MCAM), mRNA /cds=(27,1967) /gb=NM_006500 /gi=5729917 /ug=Hs.211579 /len=3583	NM_006500	Hs.211579	NP_006491
3218	0.049308	mitochondrion, complete genome	NC_001807		
3247	0.002294	602410168F1 NIH_MGC_92 cDNA clone IMAGE:4538560 5', mRNA sequence /clone=IMAGE:4538560 /clone_end=5' /gb=BG394022 /gi=13287470 /ug=Hs.421597 /len=1059	BG394022	Hs.421597	
3280	5.98E-04	RETROVIRUS-RELATED POLYPROTEIN	P11369		
3283	0.036549	PTD015	AF092136		NP_054759
3289	0.028428	likely ortholog of mouse hepatoma-derived growth factor, related protein 3 (HDGFRP3), mRNA /cds=(156,767) /gb=NM_016073 /gi=21359902 /ug=Hs.127842 /len=1973	NM_016073	Hs.127842	NP_057157
3298	0.026653	monocyte/neutrophil elastase inhibitor	AF053630		
3333	0.028428	SH3-domain kinase binding protein 1 (SH3KBP1), mRNA /cds=(292,2289) /gb=NM_031892 /gi=13994241 /ug=Hs.153260 /len=3348	NM_031892	Hs.153260	NP_114098
3334	0.038855	cDNA: FLJ23307 fis, clone HEP11549, highly similar to AF041037 novel antagonist of FGF signaling (sprouty-1) mRNA. /gb=AK026960 /gi=10439945 /ug=Hs.88044 /len=2520	AK026960	Hs.88044	
3349	0.048643	protein phosphatase 2C beta	AJ005458		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3372	0.009313	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3 (SLC11A3), mRNA /cds=(315,2030) /gb=NM_014585 /gi=19923794 /ug=Hs.5944 /len=3333	NM_014585	Hs.5944	NP_055400
3386	0.038855	Yes-associated protein 1, 65kDa (YAP1), mRNA /cds=(250,1614) /gb=NM_006106 /gi=20986484 /ug=Hs.84520 /len=5128	NM_006106	Hs.84520	NP_006097
3443	0.046501	guanylate kinase 1 (GUK1), mRNA /cds=(225,818) /gb=NM_000858 /gi=20127414 /ug=Hs.3764 /len=1082	NM_000858	Hs.3764	NP_000849
3445	0.049308	mRNA; cDNA DKFZp434A1520 (from clone DKFZp434A1520); partial cds /cds=(1,551) /gb=AL137544 /gi=6808224 /ug=Hs.406722 /len=2775	AL137544	Hs.406722	
3482	0.00684	proteasome (prosome, macropain) 26S subunit, ATPase, 5 (PSMC5), mRNA /cds=(42,1262) /gb=NM_002805 /gi=24497434 /ug=Hs.79387 /len=1332	NM_002805	Hs.79387	NP_002796
3510	0.016648	adenylate kinase 3 like 1 (AK3L1), mRNA /cds=(141,824) /gb=NM_016282 /gi=19923436 /ug=Hs.43436 /len=2642	NM_016282	Hs.43436	NP_057366
3518	0.022757	hypothetical protein FLJ23548 (FLJ23548), mRNA /cds=(204,713) /gb=NM_024590 /gi=13375780 /ug=Hs.22895 /len=1871	NM_024590	Hs.22895	NP_078866
3521	0.004961	ubiquitin-like, containing PHD and RING finger domains 2 (URF2), transcript variant 1, mRNA /cds=(341,1852) /gb=NM_152306 /gi=23312361 /ug=Hs.348602 /len=3720	NM_152306	Hs.348602	NP_690856
3532	0.020453	enabled (Drosophila) (ENAH), mRNA /cds=(77,646) /gb=NM_018212 /gi=8922657 /ug=Hs.14838 /len=2943	NM_018212	Hs.14838	NP_060682
3534	0.004205	hypothetical protein FLJ22875 (FLJ22875), mRNA /cds=(152,634) /gb=NM_032231 /gi=15638951 /ug=Hs.406548 /len=1019	NM_032231	Hs.406548	NP_115607
3536	0.038855	mRNA for KIAA1367 protein, partial cds. /cds=(1,1741) /gb=AB037788 /gi=7243114 /ug=Hs.224961 /len=4196	AB037788	Hs.224961	
3548	0.030302	eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=NM_001568 /gi=4503520 /ug=Hs.106673 /len=1510	NM_001568	Hs.106673	NP_001559
3570	0.020453	PTEN (PTEN) gene, exons 3 through 5	AF143314		
3572	0.021876	KIAA0171 gene product (KIAA0171)	NM_014666		NP_055481

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3580	0.020453	te65d01.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2091553 3', mRNA sequence /clone=IMAGE:2091553 /clone_end=3' /gb=AI377292 /gi=4187145 /ug=Hs.410753 /len=238	AI377292	Hs.410753	
3597	0.041279	hypothetical protein FLJ20152 (FLJ20152), mRNA /cds=(217,1287) /gb=NM_019000 /gi=21361616 /ug=Hs.82273 /len=2989	NM_019000	Hs.82273	NP_061873
3602	0.032277	thioredoxin-like 2 (TXNL2), mRNA /cds=(5,1012) /gb=NM_006541 /gi=5730103 /ug=Hs.42644 /len=1942	NM_006541	Hs.42644	NP_006532
3609	0.012525	mortality factor 4 like 1 (MORF4L1), mRNA /cds=(132,1103) /gb=NM_006791 /gi=5803101 /ug=Hs.6353 /len=1766	NM_006791	Hs.6353	NP_006782
3617	0.032277	microtubule associated testis specific serine/threonine protein kinase (MAST205), mRNA /cds=(284,5488) /gb=NM_015112 /gi=14149670 /ug=Hs.101474 /len=5737	NM_015112	Hs.101474	NP_055927
3623	0.014461	cDNA FLJ14089 fis, clone MAMMA1000257. /gb=AK024151 /gi=10436462 /ug=Hs.306668 /len=1730	AK024151	Hs.306668	
3727	0.01911	Sec7p-like protein mRNA, partial cds. /cds=(1,801) /gb=U59752 /gi=1465756 /ug=Hs.8517 /len=997	U59752	Hs.8517	
3740	0.010816	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase) (MTHFS), mRNA /cds=(14,625) /gb=NM_006441 /gi=5453745 /ug=Hs.118131 /len=857	NM_006441	Hs.118131	NP_006432
3761	0.020453	peroxisomal acyl-coenzyme A oxidase	S69189		NP_009223
3777	0.017843	galactosidase, alpha (GLA), mRNA /cds=(61,1350) /gb=NM_000169 /gi=4504008 /ug=Hs.69089 /len=1350	NM_000169	Hs.69089	NP_000160
3787	0.034358	secretory leukocyte protease inhibitor (antileukoprotease) (SLPI), mRNA /cds=(23,421) /gb=NM_003064 /gi=15834622 /ug=Hs.251754 /len=598	NM_003064	Hs.251754	NP_003055
3793	0.043827	myosin, light polypeptide 5, regulatory (MYL5), mRNA /cds=(106,627) /gb=NM_002477 /gi=4505304 /ug=Hs.170482 /len=661	NM_002477	Hs.170482	NP_002468
3794	0.041279	coatamer protein complex, subunit alpha (COPA), mRNA /cds=(467,4141) /gb=NM_004371 /gi=6996002 /ug=Hs.75887 /len=5064	NM_004371	Hs.75887	NP_004362

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3804	0.008631	thymidine kinase 1, soluble (TK1), mRNA /cds=(58,762) /gb=NM_003258 /gi=4507518 /ug=Hs.105097 /len=1421	NM_003258	Hs.105097	NP_003249
3806	0.032277	period 1 (Drosophila) (PER1), mRNA /cds=(188,4060) /gb=NM_002616 /gi=4505712 /ug=Hs.68398 /len=4656	NM_002616	Hs.68398	NP_002607
3830	0.012525	eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961	NM_001959	Hs.421608	NP_066944
3835	5.98E-04	NEL-like 2 (chicken) (NELL2), mRNA /cds=(97,2547) /gb=NM_006159 /gi=5453765 /ug=Hs.79389 /len=3198	NM_006159	Hs.79389	NP_006150
3844	0.020453	CGI-101 protein (F-LAN-1), mRNA /cds=(7,636) /gb=NM_016041 /gi=7705603 /ug=Hs.286131 /len=1123	NM_016041	Hs.286131	NP_057125
3846	0.032788	myosin light chain 1 slow a (MLC1SA), mRNA /cds=(48,674) /gb=NM_002475 /gi=17986280 /ug=Hs.90318 /len=778	NM_002475	Hs.90318	NP_002466
3882	0.049308	zinc finger protein 207 (ZNF207), mRNA /cds=(203,1639) /gb=NM_003457 /gi=4508016 /ug=Hs.62112 /len=2347	NM_003457	Hs.62112	NP_003448
3883	0.028428	Meis1, myeloid ecotropic viral integration site 1 (mouse) (MEIS1), mRNA /cds=(66,1238) /gb=NM_002398 /gi=4505150 /ug=Hs.170177 /len=2511	NM_002398	Hs.170177	NP_002389
3907	0.030302	Ig superfamily protein (Z39IG), mRNA /cds=(46,1245) /gb=NM_007268 /gi=6005957 /ug=Hs.8904 /len=1787	NM_007268	Hs.8904	NP_009199
3911	0.017843	mitochondrion, complete genome	NC_001807		
3921	0.003552	ALFY (ALFY), mRNA /cds=(231,10811) /gb=NM_014991 /gi=25014113 /ug=Hs.198135 /len=10811	NM_014991	Hs.198135	NP_848700
3923	0.01911	prepro insulin-like growth factor-I (IGF-I) gene, exon 1	M59812		
3958	0.016648	CGI-150 protein (CGI-150), mRNA /cds=(202,1716) /gb=NM_016080 /gi=7705645 /ug=Hs.279061 /len=2580	NM_016080	Hs.279061	NP_057164
4000	0.00145	KIAA1156	AB032982		NP_055665
4014	0.020453	mRNA; cDNA DKFZp667O1616 (from clone DKFZp667O1616) /gb=AL713722 /gi=19584452 /ug=Hs.365655 /len=1773	AL713722	Hs.365655	



Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4017	0.015521	Ras association (RalGDS/AF-6) domain family 2 (RASSF2), transcript variant 1, mRNA /cds=(197,1177) /gb=NM_014737 /gi=7661963 /ug=Hs.80905 /len=5426	NM_014737	Hs.80905	NP_739580
4036	0.041279	IDN3 protein (IDN3), transcript variant A, mRNA /cds=(363,7160) /gb=NM_133433 /gi=19718748 /ug=Hs.225767 /len=8124	NM_133433	Hs.225767	NP_597677
4064	0.00684	ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413	NM_024292	Hs.13836	NP_077268
4068	0.00684	hypothetical protein PRO2013 (PRO2013), mRNA /cds=(136,381) /gb=NM_021243 /gi=24308272 /ug=Hs.238205 /len=876	NM_021243	Hs.238205	
4103	0.013463	protein kinase C, nu (PRKCN), mRNA /cds=(556,3228) /gb=NM_005813 /gi=6563384 /ug=Hs.143460 /len=5792	NM_005813	Hs.143460	NP_005804
4106	0.030302	pre-B-cell colony-enhancing factor (PBEF), mRNA /cds=(28,1503) /gb=NM_005746 /gi=5031976 /ug=Hs.239138 /len=2376	NM_005746	Hs.239138	NP_005737
4115	0.011644	WNT1 inducible signaling pathway protein 3 (WISP3), transcript variant 1, mRNA /cds=(111,1175) /gb=NM_003880 /gi=18491002 /ug=Hs.194678 /len=1307	NM_003880	Hs.194678	NP_569080
4121	0.010816	natural killer cell enhancing factor (NKEFA)	L19184		NP_002565
4122	0.030302	serologically defined colon cancer antigen 10 (SDCCAG10), mRNA /cds=(482,1600) /gb=NM_005869 /gi=5031958 /ug=Hs.23557 /len=1857	NM_005869	Hs.23557	NP_005860
4129	0.036549	UI-H-DT0-aue-f-11-0-UI.s1 NCI_CGAP_DT0 cDNA clone IMAGE:5868298 3', mRNA sequence /clone=IMAGE:5868298 /clone_end=3' /gb=BQ030407 /gi=19765686 /ug=Hs.374637 /len=991	BQ030407	Hs.374637	
4145	0.014461	RAB10, member RAS oncogene family (RAB10), mRNA /cds=(91,693) /gb=NM_016131 /gi=7705848 /ug=Hs.236494 /len=3164	NM_016131	Hs.236494	NP_057215
4161	0.032277	sarcolemmal associated protein (SLAP1) mRNA, complete cds	U21155		
4206	0.021876	ring finger protein 4 (RNF4), mRNA /cds=(271,843) /gb=NM_002938 /gi=4506560 /ug=Hs.66394 /len=2918	NM_002938	Hs.66394	NP_002929

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4217	0.032277	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D), transcript variant 1, mRNA /cds=(198,2141) /gb=NM_032378 /gi=25453473 /ug=Hs.334798 /len=2216	NM_032378	Hs.334798	NP_115754
4246	0.037211	hypothetical protein MGC10471 (MGC10471), mRNA /cds=(227,1417) /gb=NM_030818 /gi=13540613 /ug=Hs.24998 /len=1688	NM_030818	Hs.24998	NP_110445
4257	0.020453	leucine proline-enriched proteoglycan (leprecan) 1 (LEPRE1), mRNA /cds=(42,2456) /gb=NM_022356 /gi=21361917 /ug=Hs.10114 /len=2993	NM_022356	Hs.10114	NP_071751
4286	0.024972	cartilage specific proteoglycan	X17406		NP_037359
4294	0.041279	hypothetical protein FLJ20729 (FLJ20729), mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821	NM_017953	Hs.5111	NP_060423
4307	0.038855	HT015 protein (HT015)	AF223466		NP_061049
4315	0.038855	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa (POLR2L), mRNA /cds=(22,225) /gb=NM_021128 /gi=14589956 /ug=Hs.441072 /len=392	NM_021128	Hs.441072	NP_066951
4353	0.046501	splicing factor, arginine/serine-rich 7, 35kDa (SFRS7), mRNA /cds=(54,467) /gb=NM_006276 /gi=24415993 /ug=Hs.184167 /len=2754	NM_006276	Hs.184167	NP_006267
4357	0.032277	hypothetical protein PRO1580 (PRO1580), mRNA /cds=(763,1524) /gb=NM_018502 /gi=23346636 /ug=Hs.270863 /len=1859	NM_018502	Hs.270863	NP_060972
4364	0.026653	oxysterol binding protein-like 8 (OSBPL8), mRNA /cds=(481,3150) /gb=NM_020841 /gi=22035617 /ug=Hs.109694 /len=7239	NM_020841	Hs.109694	NP_065892
4385	0.046501	cyclin L ania-6a (LOC57018), mRNA /cds=(55,1635) /gb=NM_020307 /gi=9945319 /ug=Hs.4859 /len=2076	NM_020307	Hs.4859	NP_064703
4389	0.00299	ADP-ribosylation factor 3 (ARF3)	NM_001659		NP_001650
4395	0.034358	hypothetical protein LOC51255 (LOC51255), mRNA /cds=(31,492) /gb=NM_016494 /gi=24475978 /ug=Hs.11156 /len=601	NM_016494	Hs.11156	NP_057578
4407	0.015521	15 kDa selenoprotein (SEP15), mRNA /cds=(5,493) /gb=NM_004261 /gi=20127464 /ug=Hs.90606 /len=1519	NM_004261	Hs.90606	NP_004252
4419	0.011644	KIAA0742	AB018285		NP_060903

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4421	0.041279	sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA /cds=(46,2430) /gb=NM_005065 /gi=19923668 /ug=Hs.181300 /len=7885	NM_005065	Hs.181300	NP_005056
4440	0.007397	alcohol dehydrogenase 5 (class III), chi polypeptide (ADH5), mRNA /cds=(163,1287) /gb=NM_000671 /gi=11496890 /ug=Hs.78989 /len=2496	NM_000671	Hs.78989	NP_000662
4443	0.005382	APEX nuclease (multifunctional DNA repair enzyme) 1 (APEX1), transcript variant 1, mRNA /cds=(333,1289) /gb=NM_001641 /gi=18375500 /ug=Hs.73722 /len=1574	NM_001641	Hs.73722	NP_542380
4448	0.030302	exostoses (multiple)-like 2 (EXTL2), mRNA /cds=(288,1280) /gb=NM_001439 /gi=14149608 /ug=Hs.61152 /len=2833	NM_001439	Hs.61152	NP_001430
4475	0.046501	RNA binding motif protein 8B (RBM8B)	AF231512		
4476	0.021876	adaptor-related protein complex 3, beta 1 subunit (AP3B1), mRNA /cds=(138,3422) /gb=NM_003664 /gi=24638436 /ug=Hs.155172 /len=4021	NM_003664	Hs.155172	NP_003655
4500	0.026653	X2 box repressor	U22680		
4509	0.032277	likely ortholog of mouse deleted in polyposis 1 (DP1), mRNA /cds=(38,595) /gb=NM_005669 /gi=24307896 /ug=Hs.178112 /len=3000	NM_005669	Hs.178112	NP_005660
4516	0.043827	putative cyclin G1 interacting protein (CG1I), mRNA /cds=(31,495) /gb=NM_006349 /gi=5453616 /ug=Hs.10028 /len=725	NM_006349	Hs.10028	NP_006340
4524	0.049308	ribosomal protein S23 (RPS23), mRNA /cds=(32,463) /gb=NM_001025 /gi=14790142 /ug=Hs.3463 /len=506	NM_001025	Hs.3463	NP_001016
4551	7.33E-04	mitochondrion, complete genome	NC_001807		
4552	0.032277	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa (TAF5L), mRNA /cds=(98,1867) /gb=NM_014409 /gi=21269865 /ug=Hs.26782 /len=3065	NM_014409	Hs.26782	NP_055224
4556	0.008631	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL), mRNA /cds=(52,2595) /gb=NM_002863 /gi=4506352 /ug=Hs.771 /len=2643	NM_002863	Hs.771	NP_002854

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4570	0.016648	hypothetical protein KIAA0758 protein, partial cds	AB018301		NP_056049
4571	0.003866	chromosome 1 open reading frame 13 (C1orf13), mRNA /cds=(45,1007) /gb=NM_030769 /gi=13540532 /ug=Hs.23756 /len=1552	NM_030769	Hs.23756	NP_110396
4580	0.036549	zinc finger protein 208 (ZNF208), mRNA /cds=(1,3504) /gb=NM_007153 /gi=6005975 /ug=Hs.55452 /len=3504	NM_007153	Hs.55452	NP_009084
4583	0.028428	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein) (RSN), mRNA /cds=(133,4416) /gb=NM_002956 /gi=4506750 /ug=Hs.31638 /len=5857	NM_002956	Hs.31638	NP_002947
4584	8.10E-04	Rho-associated, coiled-coil containing protein kinase 1 (ROCK1), mRNA /cds=(1,4065) /gb=NM_005406 /gi=4885582 /ug=Hs.17820 /len=4065	NM_005406	Hs.17820	NP_005397
4601	0.043827	cDNA: FLJ21869 fis, clone HEP02442. /gb=AK025522 /gi=10438064 /ug=Hs.28465 /len=2287	AK025522	Hs.28465	
4614	9.88E-04	sperm antigen-36	AF187554		
4620	0.00145	hypothetical protein MGC3196 (MGC3196), mRNA /cds=(178,291) /gb=NM_024084 /gi=13129079 /ug=Hs.309161 /len=603	NM_024084	Hs.309161	
4690	0.030302	enthoprotin (ENTH), mRNA /cds=(102,1979) /gb=NM_014666 /gi=7661967 /ug=Hs.132853 /len=3336	NM_014666	Hs.132853	NP_055481
4701	0.024972	ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413	NM_024292	Hs.13836	NP_077268
4710	0.020453	vinculin (VCL), transcript variant meta-VCL, mRNA /cds=(86,3490) /gb=NM_014000 /gi=7669549 /ug=Hs.75350 /len=5341	NM_014000	Hs.75350	NP_054706
4737	0.002294	deoxyribonuclease II, lysosomal (DNASE2), mRNA /cds=(94,1176) /gb=NM_001375 /gi=4503348 /ug=Hs.118243 /len=1975	NM_001375	Hs.118243	NP_001366
4738	0.024972	hypothetical protein (KIAA1439)	AB037860		NP_005586
4747	0.046501	leucine zipper transcription factor-like 1 (LZTFL1), mRNA /cds=(125,1024) /gb=NM_020347 /gi=9966792 /ug=Hs.30824 /len=3384	NM_020347	Hs.30824	NP_065080
4834	0.016648	mitochondrion, complete genome	NC_001807		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4837	0.049308	UI-H-BW1-amj-g-07-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070261 3', mRNA sequence /clone=IMAGE:3070261 /clone_end=3' /gb=BF513214 /gi=11598393 /ug=Hs.445888 /len=620	BF513214	Hs.445888	
4866	0.020453	FLJ31373 fis, clone NB9N42000342 /cds=UNKNOWN /gb=AK055935 /gi=16550787 /ug=Hs.281434 /len=2472	AK055935	Hs.281434	
4885	0.046501	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
4887	0.002882	mRNA; cDNA DKFZp434N079 (from clone DKFZp434N079) /gb=AL133591 /gi=6599179 /ug=Hs.141480 /len=1965	AL133591	Hs.141480	
4915	0.036549	hypothetical protein FLJ13149 (FLJ13149), mRNA /cds=(291,2585) /gb=NM_021826 /gi=11141902 /ug=Hs.112188 /len=2836	NM_021826	Hs.112188	NP_068598
4926	0.043827	nuclear receptor coactivator 1 (NCOA1), transcript variant 2, mRNA /cds=(202,4401) /gb=NM_147223 /gi=22538456 /ug=Hs.74002 /len=4721	NM_147223	Hs.74002	NP_671766
4932	0.001915	alpha-subunit of prolyl 4-hydroxylase gene, exon 12	U14616		
4950	0.01004	mRNA for KIAA1865 protein, partial cds. /cds=(622,2793) /gb=AB058768 /gi=14017946 /ug=Hs.179260 /len=3641	AB058768	Hs.179260	
4960	0.032277	hypothetical protein FLJ20958 (FLJ20958), mRNA /cds=(141,914) /gb=NM_022102 /gi=13430855 /ug=Hs.261023 /len=1842	NM_022102	Hs.261023	NP_071385
4964	0.041279	hypothetical protein FLJ22643 (FLJ22643), mRNA /cds=(15,650) /gb=NM_024635 /gi=13375865 /ug=Hs.43579 /len=997	NM_024635	Hs.43579	NP_078911
5000	0.008631	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR), mRNA /cds=(262,888) /gb=NM_001945 /gi=4503412 /ug=Hs.799 /len=2360	NM_001945	Hs.799	NP_001936
5005	0.032277	ankyrin repeat and SOCS box-containing 1 (ASB1), mRNA /cds=(87,1094) /gb=NM_016114 /gi=22208961 /ug=Hs.153489 /len=6798	NM_016114	Hs.153489	NP_057198

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5006	0.020453	cDNA FLJ33181 fis, clone ADRGL2003684, highly similar to HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H PRECURSOR. /gb=AK090500 /gi=21748675 /ug=Hs.379218 /len=2290	AK090500	Hs.379218	
5018	0.034358	mRNA; cDNA DKFZp762B195 (from clone DKFZp762B195) /gb=AL359585 /gi=8655645 /ug=Hs.356766 /len=2183	AL359585	Hs.356766	
5046	0.007397	topoisomerase II alpha-4 (AF285159)	AAG13405		
5048	0.016648	single-stranded DNA binding protein (SSBP1), mRNA /cds=(79,525) /gb=NM_003143 /gi=4507230 /ug=Hs.923 /len=628	NM_003143	Hs.923	NP_003134
5061	0.015521	wc09c01.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:2314656 3' similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR mRNA sequence /clone=IMAGE:2314656 /clone_end=3' /gb=AI674177 /gi=4874657 /ug=Hs.200089 /len=526	AI674177	Hs.200089	
5095	0.016648	nucleoporin 62kDa (NUP62), transcript variant 1, mRNA /cds=(408,1976) /gb=NM_153719 /gi=24497608 /ug=Hs.9877 /len=3403	NM_153719	Hs.9877	NP_714941
5103	3.93E-04	signal transducer and activator of transcription 6, interleukin-4 induced (STAT6) gene, complete cds	AF417842		
5141	0.012525	ubiquitin carrier protein (E2-EPF), mRNA /cds=(60,737) /gb=NM_014501 /gi=7657045 /ug=Hs.174070 /len=890	NM_014501	Hs.174070	NP_055316
5153	0.021876	ATPase, H transporting, lysosomal 13kDa, V1 subunit G isoform 1 (ATP6V1G1), mRNA /cds=(94,450) /gb=NM_004888 /gi=20357534 /ug=Hs.90336 /len=1110	NM_004888	Hs.90336	NP_004879
5169	0.049308	tenascin	X56160		NP_002151
5204	0.00326	stathmin-like 3 (STMN3), mRNA /cds=(83,625) /gb=NM_015894 /gi=14670374 /ug=Hs.285753 /len=2255	NM_015894	Hs.285753	NP_056978
5205	8.95E-04	mRNA for KIAA1458 protein, partial cds. /cds=(22,1860) /gb=AB040891 /gi=7959176 /ug=Hs.27263 /len=5843	AB040891	Hs.27263	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5233	0.038855	ATP synthase, H transporting, mitochondrial F0 complex, subunit e (ATP5I), mRNA /cds=(64,273) /gb=NM_007100 /gi=6005716 /ug=Hs.85539 /len=336	NM_007100	Hs.85539	NP_009031
5234	0.032277	deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA /cds=(707,1528) /gb=NM_013989 /gi=7549802 /ug=Hs.154424 /len=6735	NM_013989	Hs.154424	NP_054644
5252	0.017843	stromal cell protein (LOC55974), mRNA /cds=(61,726) /gb=NM_018845 /gi=10047123 /ug=Hs.292154 /len=1316	NM_018845	Hs.292154	NP_061333
5281	0.021876	ribosomal protein L6 (RPL6), mRNA /cds=(32,898) /gb=NM_000970 /gi=16753226 /ug=Hs.409045 /len=950	NM_000970	Hs.409045	NP_000961
5308	0.020453	hypothetical protein FLJ10305 (FLJ10305), mRNA /cds=(155,1729) /gb=NM_018052 /gi=20070298 /ug=Hs.5894 /len=2235	NM_018052	Hs.5894	NP_060522
5310	0.038855	cyclin D1 (PRAD1: parathyroid adenomatosis 1) (CCND1), mRNA /cds=(210,1097) /gb=NM_053056 /gi=16950654 /ug=Hs.82932 /len=4306	NM_053056	Hs.82932	NP_444284
5359	0.026653	RAP1A, member of RAS oncogene family (RAP1A), mRNA /cds=(313,867) /gb=NM_002884 /gi=4506412 /ug=Hs.865 /len=1579	NM_002884	Hs.865	NP_002875
5388	0.013463	peroxiredoxin 1 (PRDX1), mRNA /cds=(61,660) /gb=NM_002574 /gi=4505590 /ug=Hs.180909 /len=937	NM_002574	Hs.180909	NP_002565
5395	0.046501	vesicle amine transport protein 1 (T californica) (VAT1), mRNA /cds=(57,1238) /gb=NM_006373 /gi=18379348 /ug=Hs.157236 /len=2738	NM_006373	Hs.157236	NP_006364
5407	0.046501	mRNA for exportin (tRNA) /cds=(59,2947) /gb=Y16414 /gi=2924334 /ug=Hs.380785 /len=3497	Y16414	Hs.380785	NP_009166
5408	0.030302	mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (MAP3K7IP2), transcript variant 2, mRNA /cds=(176,1786) /gb=NM_145342 /gi=21735558 /ug=Hs.109727 /len=4359	NM_145342	Hs.109727	NP_663317
5432	0.00299	zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=NM_003455 /gi=10835040 /ug=Hs.9443 /len=4053	NM_003455	Hs.9443	NP_003446

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5515	0.017843	cell cycle progression 8 protein (CPR8), mRNA /cds=(13,1140) /gb=NM_004748 /gi=4758047 /ug=Hs.82506 /len=1856	NM_004748	Hs.82506	NP_004739
5541	0.043827	DKFZP434C245 protein (DKFZP434C245), mRNA /cds=(107,1201) /gb=NM_015426 /gi=14149683 /ug=Hs.59461 /len=1359	NM_015426	Hs.59461	NP_056241
5577	0.049308	kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)) (KAI1), mRNA /cds=(182,985) /gb=NM_002231 /gi=13259537 /ug=Hs.323949 /len=1623	NM_002231	Hs.323949	NP_002222
5592	0.021876	hypothetical protein MGC12904 (MGC12904), mRNA /cds=(196,951) /gb=NM_031219 /gi=13654293 /ug=Hs.7739 /len=1143	NM_031219	Hs.7739	NP_112496
5609	0.046501	peroxisomal proliferator-activated receptor A interacting complex 285 (PRIC285), mRNA /cds=(425,6667) /gb=NM_033405 /gi=21703357 /ug=Hs.151714 /len=7804	NM_033405	Hs.151714	NP_208384
5614	0.012525	mRNA; cDNA DKFZp761J0720 (from clone DKFZp761J0720) /gb=AL833252 /gi=21733885 /ug=Hs.349845 /len=3602	AL833252	Hs.349845	
5622	0.004569	eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA /cds=(369,4559) /gb=NM_004953 /gi=4826709 /ug=Hs.433750 /len=5018	NM_004953	Hs.433750	NP_004944
5671	0.034358	EPC-1 (=M76979 PEDF;U29953;M90493)	U57446		
5672	0.046501	clone IMAGE:5265581, mRNA /gb=BC035165 /gi=23272508 /ug=Hs.400548 /len=2237	BC035165	Hs.400548	
5698	0.041279	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), mRNA /cds=(233,1489) /gb=NM_000295 /gi=21361197 /ug=Hs.297681 /len=1584	NM_000295	Hs.297681	NP_000286
5699	0.036549	laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039	NM_002295	Hs.181357	NP_002286



Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5702	0.013463	adaptor-related protein complex 3, delta 1 subunit (AP3D1), mRNA /cds=(312,3773) /gb=NM_003938 /gi=20127437 /ug=Hs.75056 /len=4950	NM_003938	Hs.75056	NP_003929
5707	0.004569	nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein (SC65), mRNA /cds=(12,1325) /gb=NM_006455 /gi=5454037 /ug=Hs.446459 /len=2347	NM_006455	Hs.446459	NP_006446
5708	0.041279	NDRG family member 4 (NDRG4), mRNA /cds=(77,1192) /gb=NM_020465 /gi=14165263 /ug=Hs.322430 /len=3241	NM_020465	Hs.322430	NP_075061
5720	0.036549	carbonic anhydrase II (CA2), mRNA /cds=(66,848) /gb=NM_000067 /gi=4557394 /ug=Hs.155097 /len=1551	NM_000067	Hs.155097	NP_000058
5745	0.017843	clone IMAGE:5299888, mRNA /gb=BC039397 /gi=24659826 /ug=Hs.112237 /len=1338	BC039397	Hs.112237	
5757	0.016648	ribosomal protein S3 (RPS3), mRNA /cds=(19,750) /gb=NM_001005 /gi=15718686 /ug=Hs.414990 /len=843	NM_001005	Hs.414990	NP_000996
5806	0.024972	5'-nucleotidase, cytosolic II (NT5C2), mRNA /cds=(145,1830) /gb=NM_012229 /gi=20149601 /ug=Hs.138593 /len=3364	NM_012229	Hs.138593	NP_036361
5865	0.041279	protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 1, mRNA /cds=(93,4007) /gb=NM_002838 /gi=18641346 /ug=Hs.170121 /len=5026	NM_002838	Hs.170121	NP_563580
5866	0.030302	myeloid differentiation primary response gene (88) (MYD88), mRNA /cds=(40,930) /gb=NM_002468 /gi=19923143 /ug=Hs.82116 /len=2678	NM_002468	Hs.82116	NP_002459
5869	0.046501	ATPase, Class I, type 8B, member 1 (ATP8B1), mRNA /cds=(1,3756) /gb=NM_005603 /gi=5031696 /ug=Hs.406187 /len=3756	NM_005603	Hs.406187	NP_005594
5880	0.043827	amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), mRNA /cds=(289,2046) /gb=NM_006380 /gi=18104961 /ug=Hs.84084 /len=6468	NM_006380	Hs.84084	NP_006371
5897	0.021876	destrin (actin depolymerizing factor) (DSTN), mRNA /cds=(73,570) /gb=NM_006870 /gi=6466447 /ug=Hs.408576 /len=1439	NM_006870	Hs.408576	NP_006861

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5917	0.038855	RED CELL ACID PHOSPHATASE 1, ISOZYME F (ACP1) (LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE) (ADIPOCYTE ACID PHOSPHATASE, ISOZYME ALPHA) (62% aa)	P24666		
5920	0.004569	mitochondrion, complete genome	NC_001807		
5934	0.012525	enthoprotin (ENTH), mRNA /cds=(102,1979) /gb=NM_014666 /gi=7661967 /ug=Hs.132853 /len=3336	NM_014666	Hs.132853	NP_055481
5935	8.95E-04	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530	BF814502	Hs.446594	
5936	0.003866	amine oxidase, copper containing 3 (vascular adhesion protein 1) (AOC3), mRNA /cds=(161,2452) /gb=NM_003734 /gi=6806883 /ug=Hs.198241 /len=4040	NM_003734	Hs.198241	NP_003725
5939	0.001747	BTA1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 S. cerevisiae) (BTA1), mRNA /cds=(118,5667) /gb=NM_003972 /gi=27477069 /ug=Hs.180930 /len=6345	NM_003972	Hs.180930	NP_003963
5945	1.00E-04	dermatopontin (DPT), mRNA /cds=(7,612) /gb=NM_001937 /gi=4755134 /ug=Hs.80552 /len=717	NM_001937	Hs.80552	NP_001928
5946	0.010816	son of sevenless 1	Z11574		NP_033257
5971	0.011644	UI-E-CI1-abg-f-09-0-UI.r1 UI-E-CI1 cDNA clone UI-E-CI1-abg-f-09-0-UI 5', mRNA sequence /clone=UI-E-CI1-abg-f-09-0-UI /clone_end=5' /gb=BM691540 /gi=19004798 /ug=Hs.172047 /len=1039	BM691540	Hs.172047	
5974	0.032277	KIAA0266 gene product (KIAA0266), mRNA /cds=(734,3034) /gb=NM_021645 /gi=11063982 /ug=Hs.127376 /len=5585	NM_021645	Hs.127376	NP_067677
5975	7.33E-04	cell-line RPMI 8226 chloride ion current inducer protein I(Cln) gene,	AF232225		
5976	1.81E-04	ox06a01.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:1655496 3' similar to gb:M86849 GAP JUNCTION BETA-2 PROTEIN mRNA sequence /clone=IMAGE:1655496 /clone_end=3' /gb=AI033469 /gi=3254422 /ug=Hs.386279 /len=551	AI033469	Hs.386279	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6006	0.032277	ribosomal protein L23a (RPL23A), mRNA /cds=(22,492) /gb=NM_000984 /gi=17105393 /ug=Hs.419463 /len=546	NM_000984	Hs.419463	NP_000975
6007	0.01911	similar to 3-HYDROXYISOBUTYRATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (HIBADH) (H. sapiens) (LOC136773), mRNA	XM_059866		
6020	0.00274	cDNA FLJ37774 fis, clone BRHIP2026021, highly similar to Mus musculus formin binding protein 30 mRNA. /gb=AK095093 /gi=21754285 /ug=Hs.119533 /len=2767	AK095093	Hs.119533	
6031	0.036549	ER-resident protein ERdj5 (ERdj5), mRNA /cds=(416,2797) /gb=NM_018981 /gi=24308126 /ug=Hs.1098 /len=4193	NM_018981	Hs.1098	NP_061854
6032	0.038855	NOD1 protein (NOD1) gene	AF149773		
6078	0.030302	toll-like receptor 4 (TLR4), transcript variant 3, mRNA /cds=(408,2807) /gb=NM_003266 /gi=19924147 /ug=Hs.159239 /len=3934	NM_003266	Hs.159239	NP_612567
6079	0.036549	extracellular matrix protein 2, female organ and adipocyte specific (ECM2), mRNA /cds=(74,2173) /gb=NM_001393 /gi=4557542 /ug=Hs.35094 /len=3171	NM_001393	Hs.35094	NP_001384
6084	0.009313	SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=NM_032870 /gi=18699723 /ug=Hs.18368 /len=2663	NM_032870	Hs.18368	NP_116259
6133	0.020596	core promoter element binding protein (COPEB), mRNA /cds=(118,969) /gb=NM_001300 /gi=9961346 /ug=Hs.285313 /len=1470	NM_001300	Hs.285313	NP_001291
6187	0.026653	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I) (B3GAT3), mRNA /cds=(30,1037) /gb=NM_012200 /gi=12408653 /ug=Hs.26492 /len=1456	NM_012200	Hs.26492	NP_036332
6188	0.016648	phosphodiesterase 10A(PDE10A) mRNA	NM_006661		NP_006652
6205	0.028428	jumping translocation breakpoint (JTB), mRNA /cds=(433,873) /gb=NM_006694 /gi=5729888 /ug=Hs.6396 /len=1040	NM_006694	Hs.6396	NP_006685
6221	0.034358	adenylate kinase 1 (AK1), mRNA /cds=(75,659) /gb=NM_000476 /gi=4502010 /ug=Hs.76240 /len=2271	NM_000476	Hs.76240	NP_000467

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6230	0.022248	nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDT4), mRNA /cds=(191,736) /gb=NM_019094 /gi=24432097 /ug=Hs.355399 /len=3652	NM_019094	Hs.355399	NP_061967
6258	0.026653	deleted in liver cancer 1 (DLC1), mRNA /cds=(296,3571) /gb=NM_006094 /gi=6633799 /ug=Hs.8700 /len=3821	NM_006094	Hs.8700	NP_006085
6287	0.030302	uncharacterized hypothalamus protein HT007 (HT007), mRNA /cds=(228,887) /gb=NM_018480 /gi=8923801 /ug=Hs.24371 /len=1172	NM_018480	Hs.24371	NP_060950
6297	0.041279	5'-nucleotidase, cytosolic II (NT5C2), mRNA /cds=(145,1830) /gb=NM_012229 /gi=20149601 /ug=Hs.138593 /len=3364	NM_012229	Hs.138593	NP_036361
6307	0.006602	cDNA FLJ37296 fis, clone BRAMY2015420. /gb=AK094615 /gi=21753707 /ug=Hs.4983 /len=3181	AK094615	Hs.4983	
6310	0.036549	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa (EIF2S1), mRNA /cds=(100,1047) /gb=NM_004094 /gi=19923248 /ug=Hs.151777 /len=2992	NM_004094	Hs.151777	NP_004085
6311	0.002508	peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(45,542) /gb=NM_021130 /gi=10863926 /ug=Hs.401787 /len=753	NM_021130	Hs.401787	NP_066953
6334	0.008631	pilin-like transCRIPTION factor	AF122004		NP_036360
6347	0.01911	mitochondrion, complete genome	NC_001807		
6368	0.032277	gamma-aminobutyric acid (GABA) A receptor, alpha 4 (GABRA4), mRNA /cds=(39,1703) /gb=NM_000809 /gi=4557604 /ug=Hs.248112 /len=1703	NM_000809	Hs.248112	NP_000800
6386	0.034358	mitochondrion, complete genome	NC_001807		
6387	0.028428	epithelial protein lost in neoplasm beta (EPLIN), mRNA /cds=(102,2381) /gb=NM_016357 /gi=7705372 /ug=Hs.10706 /len=3655	NM_016357	Hs.10706	NP_057441
6392	0.017995	clock (mouse) (CLOCK), mRNA /cds=(339,2879) /gb=NM_004898 /gi=25777594 /ug=Hs.150602 /len=5801	NM_004898	Hs.150602	NP_004889
6396	0.041279	ADP-ribosyltransferase (NAD ; poly(ADP-ribose) polymerase)-like 2 (ADPRTL2), mRNA /cds=(150,1754) /gb=NM_005484 /gi=11496991 /ug=Hs.24284 /len=1887	NM_005484	Hs.24284	NP_005475

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6403	0.012525	glyceronephosphate O-acyltransferase (GNPAT), mRNA /cds=(158,2200) /gb=NM_014236 /gi=7657133 /ug=Hs.12482 /len=2470	NM_014236	Hs.12482	NP_055051
6407	0.003552	hypothetical protein LOC51244 (LOC51244), mRNA /cds=(340,1233) /gb=NM_016474 /gi=24475969 /ug=Hs.158006 /len=1614	NM_016474	Hs.158006	NP_057558
6412	1.61E-04	KIAA0716 gene product (KIAA0716), mRNA /cds=(192,2489) /gb=NM_014705 /gi=7662263 /ug=Hs.118140 /len=4652	NM_014705	Hs.118140	NP_055520
6414	0.026653	eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), mRNA /cds=(307,3030) /gb=NM_001418 /gi=4503538 /ug=Hs.183684 /len=3820	NM_001418	Hs.183684	NP_001409
6424	0.023381	intersectin short form	AF064243		NP_003015
6426	0.036549	microtubule-associated protein 1B (MAP1B), transcript variant 1, mRNA /cds=(223,7629) /gb=NM_005909 /gi=14165457 /ug=Hs.103042 /len=9416	NM_005909	Hs.103042	NP_114399
6428	0.036549	serologically defined colon cancer antigen 1 (SDCCAG1), mRNA /cds=(183,1271) /gb=NM_004713 /gi=4759077 /ug=Hs.388584 /len=2078	NM_004713	Hs.388584	NP_004704
6432	0.049308	protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA /cds=(167,1423) /gb=NM_002736 /gi=4506064 /ug=Hs.77439 /len=3259	NM_002736	Hs.77439	NP_002727
6439	0.038855	protein phosphatase 1, catalytic subunit, beta isoform (PPP1CB), mRNA /cds=(259,1242) /gb=NM_002709 /gi=4506004 /ug=Hs.21537 /len=3590	NM_002709	Hs.21537	NP_002700
6443	0.003866	Mlx interactor (MONDOA), mRNA /cds=(153,1733) /gb=NM_014938 /gi=7662347 /ug=Hs.52081 /len=4339	NM_014938	Hs.52081	NP_055753
6444	0.034358	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta) (PPP3CB), mRNA /cds=(117,1691) /gb=NM_021132 /gi=11036639 /ug=Hs.151531 /len=3079	NM_021132	Hs.151531	NP_066955
6475	0.003866	ubiquitin-conjugating enzyme (PUBC1) mRNA, complete cds	AF317220		NP_003330
6476	0.026653	ELK3, ETS-domain protein (SRF accessory protein 2), FLJ22425 fis, clone HRC08686 (AK026078.1)	AK026078	Hs.288555	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6496	0.028428	TATA element modulatory factor 1 (TMF1), mRNA /cds=(1,3282) /gb=NM_007114 /gi=6005903 /ug=Hs.267632 /len=3282	NM_007114	Hs.267632	NP_009045
6529	1.61E-04	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA /cds=(95,1048) /gb=NM_020529 /gi=10092618 /ug=Hs.81328 /len=1550	NM_020529	Hs.81328	NP_065390
6530	0.036549	pleckstrin domain containing, family A (phosphoinositide binding specific) member 4 (PLEKHA4), mRNA /cds=(526,2865) /gb=NM_020904 /gi=10190743 /ug=Hs.9469 /len=3056	NM_020904	Hs.9469	NP_065955
6537	0.008631	selenoprotein P, plasma, 1 (SEPP1), mRNA /cds=(37,1182) /gb=NM_005410 /gi=4885590 /ug=Hs.275775 /len=2038	NM_005410	Hs.275775	NP_005401
6550	0.020453	t-complex-associated-testis-expressed 1-like 1 (TCTEL1), mRNA /cds=(1,342) /gb=NM_006519 /gi=5730084 /ug=Hs.266940 /len=713	NM_006519	Hs.266940	NP_006510
6551	0.034358	URB mRNA, complete cds /cds=(146,2998) /gb=AF506819 /gi=21039408 /ug=Hs.356289 /len=3320	AF506819	Hs.356289	
6554	0.043827	mitochondrial ribosomal protein L13 (MRPL13), nuclear gene encoding mitochondrial protein, mRNA /cds=(287,823) /gb=NM_014078 /gi=21265072 /ug=Hs.333823 /len=1086	NM_014078	Hs.333823	NP_054797
6565	0.036549	PTK9 protein tyrosine kinase 9 (PTK9), mRNA /cds=(61,1113) /gb=NM_002822 /gi=4506274 /ug=Hs.82643 /len=3000	NM_002822	Hs.82643	NP_002813
6571	0.020453	KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NM_015216 /gi=7662117 /ug=Hs.26179 /len=5814	NM_015216	Hs.26179	NP_056031
6574	0.01004	RCC1	D00591		
6592	0.028428	methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,1111) /gb=NM_006636 /gi=13699869 /ug=Hs.154672 /len=2154	NM_006636	Hs.154672	NP_006627

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6594	0.034358	lactate dehydrogenase A (LDHA), mRNA /cds=(98,1096) /gb=NM_005566 /gi=5031856 /ug=Hs.2795 /len=1661	NM_005566	Hs.2795	NP_005557
6609	0.012525	fibroblast growth factor 2 (basic) (FGF2), mRNA /cds=(302,934) /gb=NM_002006 /gi=15451897 /ug=Hs.284244 /len=6802	NM_002006	Hs.284244	NP_001997
6610	0.005835	Similar to RIKEN cDNA 3830613O22 gene, clone IMAGE:5551209, mRNA, partial cds /cds=(282,4079) /gb=BC035645 /gi=23272851 /ug=Hs.356876 /len=4079	BC035645	Hs.356876	
6651	0.001915	tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), mRNA /cds=(96,941) /gb=NM_003810 /gi=23510439 /ug=Hs.83429 /len=1776	NM_003810	Hs.83429	NP_003801
6656	0.046501	protein phosphatase 1, regulatory (inhibitor) subunit 2 (PPP1R2), mRNA /cds=(235,852) /gb=NM_006241 /gi=19923357 /ug=Hs.267819 /len=3355	NM_006241	Hs.267819	NP_006232
6673	0.049308	cAMP responsive element binding protein 3 (luman) (CREB3), mRNA /cds=(439,1554) /gb=NM_006368 /gi=22219461 /ug=Hs.287921 /len=1837	NM_006368	Hs.287921	NP_006359
6692	3.93E-04	mitochondrial ribosomal protein S18B (MRPS18B), nuclear gene encoding mitochondrial protein, mRNA /cds=(38,814) /gb=NM_014046 /gi=16554601 /ug=Hs.274417 /len=1439	NM_014046	Hs.274417	NP_054765
6727	0.036549	ribosomal protein L13 (RPL13), transcript variant 2, mRNA /cds=(238,873) /gb=NM_033251 /gi=15431294 /ug=Hs.431392 /len=1296	NM_033251	Hs.431392	NP_150254
6759	0.036549	signal recognition particle 19kDa (SRP19), mRNA /cds=(82,516) /gb=NM_003135 /gi=4507212 /ug=Hs.2943 /len=894	NM_003135	Hs.2943	NP_003126
6773	0.041279	hypothetical protein FLJ14834 (FLJ14834), mRNA /cds=(326,1237) /gb=NM_032849 /gi=21361885 /ug=Hs.62905 /len=2342	NM_032849	Hs.62905	NP_116238

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6793	0.036549	transforming growth factor, beta receptor III (betaglycan, 300kDa) (TGFB3), mRNA /cds=(349,2898) /gb=NM_003243 /gi=4507470 /ug=Hs.342874 /len=4208	NM_003243	Hs.342874	NP_003234
6813	0.034358	constitutive photomorphogenic protein (COP1), mRNA /cds=(1,2196) /gb=NM_022457 /gi=21359962 /ug=Hs.105737 /len=2196	NM_022457	Hs.105737	NP_071902
6822	0.023381	MSTP031 protein (MSTP031), mRNA /cds=(663,1091) /gb=NM_032035 /gi=14042961 /ug=Hs.105689 /len=1284	NM_032035	Hs.105689	NP_114424
6825	0.043827	hypothetical protein MGC4400 (MGC4400), mRNA /cds=(381,1817) /gb=NM_032679 /gi=14249251 /ug=Hs.130891 /len=3067	NM_032679	Hs.130891	NP_116068
6846	0.049308	mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant A, mRNA /cds=(306,2045) /gb=NM_003188 /gi=21735560 /ug=Hs.7510 /len=2912	NM_003188	Hs.7510	NP_663306
6943	0.007397	hypothetical protein FLJ10849 (FLJ10849), mRNA /cds=(94,1383) /gb=NM_018243 /gi=8922711 /ug=Hs.8768 /len=2845	NM_018243	Hs.8768	NP_060713
6970	0.043827	neuroblastoma apoptosis-related RNA-binding protein (CUGBP2) gene, exons 10, 11a, 11b, 12, 13a, 13b, 14, and complete cds, alternatively spliced	AF295068		
6989	0.036549	transmembrane 9 superfamily member 1 (TM9SF1), mRNA /cds=(35,1855) /gb=NM_006405 /gi=21361314 /ug=Hs.91586 /len=2138	NM_006405	Hs.91586	NP_006396
6998	0.049308	DKFZp434P0235 (from clone DKFZp434P0235) /cds=UNKNOWN /gb=AL117519 /gi=5912035 /ug=Hs.34348 /len=1124	AL117519	Hs.34348	NP_849157
6999	0.046501	ring finger protein 20 (RNF20), mRNA /cds=(91,3018) /gb=NM_019592 /gi=16554452 /ug=Hs.168095 /len=3936	NM_019592	Hs.168095	NP_062538
7045	0.00684	methionine adenosyltransferase II, beta (MAT2B), mRNA /cds=(73,1077) /gb=NM_013283 /gi=20127525 /ug=Hs.54642 /len=2054	NM_013283	Hs.54642	NP_037415
7051	0.014461	guanine nucleotide binding protein 11 (GNG11), mRNA /cds=(352,573) /gb=NM_004126 /gi=20127455 /ug=Hs.83381 /len=884	NM_004126	Hs.83381	NP_004117



Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7052	0.043827	SUMO-1-specific protease (SUSP1), mRNA /cds=(1,3339) /gb=NM_015571 /gi=7662311 /ug=Hs.27197 /len=4210	NM_015571	Hs.27197	NP_056386
7068	0.020453	KIAA1128 protein (KIAA1128), mRNA /cds=(553,2253) /gb=NM_018999 /gi=24308130 /ug=Hs.81897 /len=7248	NM_018999	Hs.81897	NP_061872
7069	0.003866	adenosine monophosphate deaminase (isoform E) (AMPD3), mRNA /cds=(345,2675) /gb=NM_000480 /gi=4502078 /ug=Hs.83918 /len=3915	NM_000480	Hs.83918	NP_000471
7077	0.00299	mitochondrion, complete genome	NC_001807		
7078	0.011644	KIAA0438 gene product (KIAA0438), mRNA /cds=(118,2244) /gb=NM_014819 /gi=7662123 /ug=Hs.279849 /len=4765	NM_014819	Hs.279849	NP_055634
7099	0.030302	cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, mRNA /cds=(105,680) /gb=NM_001791 /gi=16357470 /ug=Hs.146409 /len=2183	NM_001791	Hs.146409	NP_426359
7151	0.034358	DNA (cytosine-5-)-methyltransferase 1 (DNMT1), mRNA /cds=(238,5088) /gb=NM_001379 /gi=4503350 /ug=Hs.77462 /len=5434	NM_001379	Hs.77462	NP_001370
7165	0.043827	zinc finger protein 25 (KOX 19) (ZNF25), mRNA /cds=(106,1476) /gb=NM_145011 /gi=24462252 /ug=Hs.5856 /len=3736	NM_145011	Hs.5856	NP_659448
7175	0.01911	AGENCOURT_6853421 NIH_MGC_99 cDNA clone IMAGE:5926418 5', mRNA sequence /clone=IMAGE:5926418 /clone_end=5' /gb=BQ064669 /gi=19893520 /ug=Hs.380699 /len=969	BQ064669	Hs.380699	
7176	0.016648	tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(95,613) /gb=NM_003295 /gi=4507668 /ug=Hs.401448 /len=830	NM_003295	Hs.401448	NP_003286
7186	0.026653	chromosome 9 open reading frame 7 (C9orf7), mRNA /cds=(59,577) /gb=NM_017586 /gi=8922115 /ug=Hs.119285 /len=2695	NM_017586	Hs.119285	NP_060056
7236	0.013463	eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=NM_001568 /gi=4503520 /ug=Hs.106673 /len=1510	NM_001568	Hs.106673	NP_001559
7268	0.028428	cDNA: FLJ21904 fis, clone HEP03585. /gb=AK025557 /gi=10438108 /ug=Hs.110771 /len=2224	AK025557	Hs.110771	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7272	0.034358	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4 (FLJ11021), mRNA /cds=(767,1375) /gb=NM_023012 /gi=20127619 /ug=Hs.81648 /len=1878	NM_023012	Hs.81648	NP_075388
7278	0.024972	KIAA0648 protein (KIAA0648), mRNA /cds=(232,4125) /gb=NM_015200 /gi=22094120 /ug=Hs.31921 /len=6744	NM_015200	Hs.31921	NP_056015
7288	0.028428	KIAA0800 gene product (KIAA0800), mRNA /cds=(169,4692) /gb=NM_014703 /gi=7662315 /ug=Hs.118738 /len=5984	NM_014703	Hs.118738	NP_055518
7314	0.01004	chromosome 11 open reading frame 10 (C11orf10), mRNA /cds=(56,295) /gb=NM_014206 /gi=7656933 /ug=Hs.90918 /len=418	NM_014206	Hs.90918	NP_055021
7320	0.00274	RNA-binding region (RNP1, RRM) containing 4 (RNPC4), mRNA /cds=(187,1461) /gb=NM_018107 /gi=21361701 /ug=Hs.4997 /len=2442	NM_018107	Hs.4997	NP_060577
7321	0.021876	translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523) /gb=NM_006335 /gi=5454119 /ug=Hs.20716 /len=1645	NM_006335	Hs.20716	NP_006326
7349	0.030302	dermatopontin (DPT), mRNA /cds=(7,612) /gb=NM_001937 /gi=4755134 /ug=Hs.80552 /len=717	NM_001937	Hs.80552	NP_001928
7356	0.041279	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) (CLU), mRNA /cds=(48,1397) /gb=NM_001831 /gi=4502904 /ug=Hs.75106 /len=1676	NM_001831	Hs.75106	NP_001822
7357	0.041279	chromosome 6 open reading frame 33 (C6orf33), mRNA /cds=(165,1229) /gb=NM_133367 /gi=19115959 /ug=Hs.239388 /len=4650	NM_133367	Hs.239388	NP_588608
7363	0.043827	small acidic protein (SMAP), mRNA /cds=(137,688) /gb=NM_014267 /gi=20070245 /ug=Hs.78050 /len=1504	NM_014267	Hs.78050	NP_055082
7369	0.012525	cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA /cds=(206,2926) /gb=NM_001792 /gi=14589888 /ug=Hs.161 /len=4122	NM_001792	Hs.161	NP_001783
7378	0.001915	regulator of G-protein signalling 10 (RGS10), mRNA /cds=(44,547) /gb=NM_002925 /gi=11184225 /ug=Hs.82280 /len=664	NM_002925	Hs.82280	NP_002916

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7387	0.032261	ribosomal protein L4 (RPL4), mRNA /cds=(57,1340) /gb=NM_000968 /gi=16579884 /ug=Hs.286 /len=1449	NM_000968	Hs.286	NP_000959
7405	0.028428	MAGE-E1 protein (MAGE-E1), mRNA /cds=(146,1390) /gb=NM_030801 /gi=13540587 /ug=Hs.7457 /len=2997	NM_030801	Hs.7457	NP_803881
7414	0.0062	tetraspanin similar to TM4SF9 (DC-TM4F2), mRNA /cds=(79,891) /gb=NM_030927 /gi=13569888 /ug=Hs.101395 /len=2556	NM_030927	Hs.101395	NP_112189
7418	0.026653	similar to KIAA1795 protein (H. sapiens) (LOC133247), mRNA	XM_059632		
7483	0.009313	hypothetical gene supported by XM_074428 (LOC123440), mRNA	XM_074428		
7508	0.046501	mRNA for RCC1-like protein (TD-60 gene) /cds=(236,1804) /gb=AJ421269 /gi=27526612 /ug=Hs.284146 /len=4114	AJ421269	Hs.284146	NP_061185
7510	0.015521	hypothetical protein MGC14327 (MGC14327), mRNA /cds=(225,635) /gb=NM_053045 /gi=16596685 /ug=Hs.231029 /len=1576	NM_053045	Hs.231029	NP_444273
7533	0.036549	pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, mRNA /cds=(2242,3633) /gb=NM_006718 /gi=27894292 /ug=Hs.75825 /len=4816	NM_006718	Hs.75825	NP_006709
7550	0.026653	hypothetical protein FLJ20343 (FLJ20343), mRNA /cds=(19,1524) /gb=NM_017775 /gi=22547158 /ug=Hs.252692 /len=2784	NM_017775	Hs.252692	NP_060245
7564	0.026653	paired basic amino acid cleaving system 4 (PACE4), transcript variant 1, mRNA /cds=(315,3224) /gb=NM_002570 /gi=20336178 /ug=Hs.170414 /len=4553	NM_002570	Hs.170414	NP_612198
7578	0.004961	hypothetical protein DKFZp586G0123 (DKFZp586G0123), mRNA /cds=(25,315) /gb=NM_013386 /gi=9558726 /ug=Hs.24713 /len=1294	NM_013386	Hs.24713	NP_037518
7592	0.036549	KIAA1221 protein (KIAA1221), mRNA /cds=(129,4037) /gb=NM_032186 /gi=24496786 /ug=Hs.173001 /len=5531	NM_032186	Hs.173001	NP_115562
7614	0.012525	ALS2CR3 gene for amyotrophic lateral sclerosis 2, candidate 3, exon 14	AB038962		
7683	0.032277	zinc finger protein 302 (ZNF302), mRNA /cds=(337,1773) /gb=NM_018675 /gi=11034834 /ug=Hs.125287 /len=2978	NM_018675	Hs.125287	NP_061145

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7714	0.041279	hypothetical protein MGC40107 (MGC40107), mRNA /cds=(40,381) /gb=NM_152766 /gi=22749498 /ug=Hs.94316 /len=495	NM_152766	Hs.94316	NP_689979
7716	0.026653	IFNAR gene (HSIFNAR) for interferon alpha/beta receptor	X60459		
7717	0.024972	similar to putative (H. sapiens) (LOC129401), mRNA	XM_059351		
7730	0.024972	MTB (MTB) mRNA, complete cds /cds=(80,265) /gb=AF348994 /gi=28190031 /ug=Hs.333727 /len=408	AF348994	Hs.333727	NP_783321
7738	0.030302	te65d01.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2091553 3', mRNA sequence /clone=IMAGE:2091553 /clone_end=3' /gb=AI377292 /gi=4187145 /ug=Hs.410753 /len=238	AI377292	Hs.410753	
7789	0.023381	EST (DKFZp564A043 clone DKFZp564A043)	AL050007		
7851	0.032277	capillary morphogenesis protein 2 (CMG2), mRNA /cds=(46,783) /gb=NM_058172 /gi=17158002 /ug=Hs.5897 /len=2026	NM_058172	Hs.5897	NP_477520
7868	0.049308	EST(yx98h12.s1 Soares melanocyte 2NbHM cDNA clone IMAGE:269831 3')	N24829		
7923	0.043827	Tara-like protein (HRIHFB2122), transcript variant 1, mRNA /cds=(176,1957) /gb=NM_007032 /gi=20336765 /ug=Hs.40342 /len=2687	NM_007032	Hs.40342	NP_619538
7925	0.046501	EST(ng19d12.s1 NCI_CGAP_Lip2 cDNA clone IMAGE:929879 similar to contains Alu repetitive element;contains element MSR1 repetitive element)	AA501823		
7928	0.049308	hypothetical protein HSPC195 (HSPC195), mRNA /cds=(293,889) /gb=NM_016463 /gi=20070365 /ug=Hs.356509 /len=1108	NM_016463	Hs.356509	
7943	0.001915	EST (AV754618 TP cDNA clone TPGAAA04 5')	AV754618		
7992	0.004569	brain cDNA clone:QccE-22013, full insert sequence	AB060197		
8017	0.041279	secreted frizzled-related protein 5 (SFRP5), mRNA /cds=(182,1135) /gb=NM_003015 /gi=8400734 /ug=Hs.279565 /len=1905	NM_003015	Hs.279565	NP_003006
8018	9.88E-04	tubulin, gamma 1 (TUBG1), mRNA /cds=(25,1380) /gb=NM_001070 /gi=4507730 /ug=Hs.21635 /len=1568	NM_001070	Hs.21635	NP_001061

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8030	0.041279	FLJ23497 (FLJ23497), mRNA /cds=(624,1091) /gb=NM_025089 /gi=13376647 /ug=Hs.288498 /len=1929	NM_025089	Hs.288498	
8036	0.012525	mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant A, mRNA /cds=(306,2045) /gb=NM_003188 /gi=21735560 /ug=Hs.7510 /len=2912	NM_003188	Hs.7510	NP_663306
8046	0.011644	cDNA FLJ10423 fis, clone NT2RP1000259. /gb=AK001285 /gi=7022444 /ug=Hs.106909 /len=1837	AK001285	Hs.106909	
8080	0.024972	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA /cds=(252,1457) /gb=NM_002546 /gi=22547122 /ug=Hs.81791 /len=2291	NM_002546	Hs.81791	NP_002537
8137	0.038855	cartilage acidic protein 1 (CRTAC1), mRNA /cds=(319,1575) /gb=NM_018058 /gi=8922351 /ug=Hs.326444 /len=2178	NM_018058	Hs.326444	NP_060528
8163	0.041279	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa (NDUFB3), mRNA /cds=(253,549) /gb=NM_002491 /gi=4505360 /ug=Hs.109760 /len=693	NM_002491	Hs.109760	NP_002482
8182	0.049308	general transcription factor IIH, polypeptide 2, 44kDa (GTF2H2), mRNA /cds=(1,1188) /gb=NM_001515 /gi=6681761 /ug=Hs.191356 /len=1188	NM_001515	Hs.191356	NP_001506
8198	0.016648	PHD zinc finger protein XAP135 (XAP135), transcript variant 2, mRNA /cds=(222,1448) /gb=NM_133325 /gi=19747275 /ug=Hs.7759 /len=1583	NM_133325	Hs.7759	NP_579866
8199	0.005835	hypothetical protein MGC18216 (MGC18216), mRNA /cds=(2207,2374) /gb=NM_152452 /gi=22748948 /ug=Hs.104679 /len=3270	NM_152452	Hs.104679	NP_689665
8223	0.028428	FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=NM_007270 /gi=24307926 /ug=Hs.302749 /len=2517	NM_007270	Hs.302749	NP_009201
8227	0.004205	hypothetical protein FLJ20628 (FLJ20628), mRNA /cds=(23,1456) /gb=NM_017910 /gi=13435382 /ug=Hs.32356 /len=1846	NM_017910	Hs.32356	NP_060380

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8231	0.007397	peptide-histidine transporter 4 (PTR4), mRNA /cds=(59,1792) /gb=NM_145648 /gi=21717815 /ug=Hs.355660 /len=2807	NM_145648	Hs.355660	NP_663623
8240	0.022757	mitochondrion, complete genome	NC_001807		
8241	0.002161	hypothetical protein MGC3196 (MGC3196), mRNA /cds=(178,291) /gb=NM_024084 /gi=13129079 /ug=Hs.309161 /len=603	NM_024084	Hs.309161	
8243	0.023381	T-cell lymphoma invasion and metastasis 2 (TIAM2), mRNA /cds=(51,3284) /gb=NM_012454 /gi=6912703 /ug=Hs.12598 /len=4586	NM_012454	Hs.12598	NP_036586
8246	0.041279	Ras-GTPase activating protein SH3 domain-binding protein 2 (KIAA0660), mRNA /cds=(121,1569) /gb=NM_012297 /gi=19923398 /ug=Hs.433496 /len=4210	NM_012297	Hs.433496	NP_036429
8258	0.036549	EST(zb77f03.s1 Soares senescent fibroblasts NbHSF cDNA clone 309629 3')	N94450		NP_073600
8262	0.043827	HSPC166 protein (HSPC166), mRNA /cds=(19,615) /gb=NM_014186 /gi=7661827 /ug=Hs.279836 /len=1318	NM_014186	Hs.279836	NP_054905
8311	0.015521	clone IMAGE:5295441, mRNA /gb=BC043222 /gi=28175025 /ug=Hs.405253 /len=2712	BC043222	Hs.405253	
8345	0.034358	hypothetical protein FLJ35613 (FLJ35613), mRNA /cds=(126,2063) /gb=NM_173653 /gi=27734934 /ug=Hs.30022 /len=3568	NM_173653	Hs.30022	NP_775924
8395	0.043827	EST xp73h11.x1 NCI_CGAP_Ov40 cDNA clone IMAGE:2746053 3' similar to contains Alu repetitive element;contains element MER32 repetitive element ;	AW270457		
8417	0.032277	EST QV4-FT0005-110500-203-e03 FT0005	AW949100		
8432	8.95E-04	EST 7f59d09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 H.sapiens cDNA clone IMAGE:3298961 3'	BE677740		
8435	0.00274	BX099435 NCI_CGAP_Co8 cDNA clone IMAGp998M083951, mRNA sequence /clone=IMAGp998M083951_/_IMAGE:1559599 /gb=BX099435 /gi=27829993 /ug=Hs.126589 /len=659	BX099435	Hs.126589	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8443	0.004569	UI-H-EU1-bag-b-11-0-UI.s1 NCI_CGAP_Ct1 cDNA clone UI-H-EU1-bag-b-11-0-UI 3', mRNA sequence /clone=UI-H-EU1-bag-b-11-0-UI /clone_end=3' /gb=BQ448425 /gi=21251537 /ug=Hs.438826 /len=1023	BQ448425	Hs.438826	
8457	0.030302	EST (T98494 ye60e05.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:122144 3')	T98494		
8460	0.020453	AV705591 ADB cDNA clone ADBCGF11 5', mRNA sequence /clone=ADBCGF11 /clone_end=5' /gb=AV705591 /gi=10722889 /ug=Hs.287350 /len=677	AV705591	Hs.287350	
8489	0.036549	CLK4 mRNA sequence /cds=(154,1515) /gb=AF212224 /gi=9437514 /ug=Hs.406557 /len=1865	AF212224	Hs.406557	
8499	0.026653	hypothetical protein FLJ30999 (FLJ30999), mRNA /cds=(302,703) /gb=NM_152461 /gi=22748964 /ug=Hs.129166 /len=2067	NM_152461	Hs.129166	NP_689674
8500	0.036549	EST375644 MAGE resequences, MAGH. cDNA, mRNA sequence /gb=AW963571 /gi=8153407 /ug=Hs.182962 /len=672	AW963571	Hs.182962	
8501	0.021876	hypothetical protein FLJ40137 (FLJ40137), mRNA /cds=(149,1141) /gb=NM_173478 /gi=27735056 /ug=Hs.412708 /len=2241	NM_173478	Hs.412708	NP_775749
8529	0.041279	EST (602645742F1 NIH_MGC_76 clone IMAGE:4767299 5')	BG618375		
8547	0.011644	cDNA FLJ36837 fis, clone ASTRO2011422. /gb=AK094156 /gi=21753158 /ug=Hs.36475 /len=3302	AK094156	Hs.36475	
8550	0.016648	cDNA FLJ36544 fis, clone TRACH2006378. /gb=AK093863 /gi=21752807 /ug=Hs.101689 /len=2670	AK093863	Hs.101689	
8553	0.032277	EST (we35d08.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:2343087 3' similar to contains L1.t1 L1 repetitive element )	AI701473		
8570	0.024972	EST hz28e05.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3209312 3'	BE466897		
8577	0.049308	RC5-FT0194-271100-022-B06 FT0194 cDNA, mRNA sequence /gb=BF858635 /gi=12246379 /ug=Hs.270272 /len=590	BF858635	Hs.270272	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8595	0.046501	ribosomal protein L3 (RPL3), mRNA /cds=(27,1238) /gb=NM_000967 /gi=16507968 /ug=Hs.119598 /len=1311	NM_000967	Hs.119598	NP_000958
8604	0.041279	wg14b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:2365055 3', mRNA sequence /clone=IMAGE:2365055 /clone_end=3' /gb=AI800904 /gi=5366376 /ug=Hs.132105 /len=537	AI800904	Hs.132105	
8610	0.014461	EST, cDNA /gb=AW816379 /gi=7909373 /ug=Hs.335018 /len=603	AW816379	Hs.335018	
8622	0.005834	FLJ30623 fis, clone CTONG2001748 /cds=UNKNOWN /gb=AK055185 /gi=16549855 /ug=Hs.351574 /len=2870	AK055185	Hs.351574	NP_079050
8623	0.015521	cDNA FLJ31753 fis, clone NT2RI2007468. /gb=AK056315 /gi=16551681 /ug=Hs.349283 /len=2361	AK056315	Hs.349283	
8624	0.014461	mRNA; cDNA DKFZp313C0935 (from clone DKFZp313C0935) /gb=AL832706 /gi=21733285 /ug=Hs.433110 /len=3270	AL832706	Hs.433110	
8649	0.001915	nah90b12.x1 NCI_CGAP_HN19 cDNA clone IMAGE:4257766 similar to P39194 ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY. [1] ;contains Alu repetitive element;, mRNA sequence /clone=IMAGE:4257766 /gb=BG272785 /gi=12982288 /ug=Hs.440690 /len=360	BG272785	Hs.440690	
8653	0.009313	EST, cDNA /clone=DKFZp586F2021 /gb=AL047579 /gi=4728575 /ug=Hs.310753 /len=431	AL047579	Hs.310753	
8661	0.011644	UI-H-EI1-azf-b-12-0-UI.s1 NCI_CGAP_EI1 cDNA clone IMAGE:5847851 3', mRNA sequence /clone=IMAGE:5847851 /clone_end=3' /gb=BQ003897 /gi=19728797 /ug=Hs.446354 /len=1034	BQ003897	Hs.446354	
8662	0.007397	ts93d11.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2238837 3', mRNA sequence /clone=IMAGE:2238837 /clone_end=3' /gb=AI631165 /gi=4682495 /ug=Hs.196952 /len=537	AI631165	Hs.196952	
8669	0.012525	cDNA FLJ10190 fis, clone HEMBA1004753. /gb=AK001052 /gi=7022081 /ug=Hs.274546 /len=1318	AK001052	Hs.274546	



Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8673	0.005835	jun1.P1.D7 conorm cDNA 3', mRNA sequence /clone_end=3' /gb=AI535800 /gi=4449935 /ug=Hs.369112 /len=480	AI535800	Hs.369112	
8675	0.041279	UI-H-EI0-ayo-a-20-0-UI.s1 NCI_CGAP_EI0 cDNA clone IMAGE:5841307 3', mRNA sequence /clone=IMAGE:5841307 /clone_end=3' /gb=BQ004581 /gi=19729481 /ug=Hs.412459 /len=1095	BQ004581	Hs.412459	
8680	0.014457	hypothetical protein FLJ32234 (FLJ32234), mRNA /cds=(37,471) /gb=NM_152551 /gi=22749140 /ug=Hs.13366 /len=3051	NM_152551	Hs.13366	NP_689764
8685	0.036549	Similar to ubiquitin protein ligase E3A papilloma virus E6-associated protein, Angelman syndrome), clone IMAGE:4811444, mRNA /gb=BC040187 /gi=25455694 /ug=Hs.25320 /len=4823	BC040187	Hs.25320	
8686	0.005835	mRNA; cDNA DKFZp564P016 (from clone DKFZp564P016) /gb=AL049337 /gi=4500118 /ug=Hs.132571 /len=1938	AL049337	Hs.132571	
8689	0.021876	ESTs, cDNA, 3' end /clone=DKFZp434I2028 /clone_end=3' /gb=AL044007 /gi=5432235 /ug=Hs.95663 /len=535	AL044007	Hs.95663	
8695	0.038855	HNC36-1-D2.R HNC Normal Cartilage) cDNA, mRNA sequence /gb=BG924955 /gi=14319478 /ug=Hs.351383 /len=722	BG924955	Hs.351383	
8707	0.041279	tc93c11.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2073716 3' similar to contains Alu repetitive element;, mRNA sequence /clone=IMAGE:2073716 /clone_end=3' /gb=AI475669 /gi=4328714 /ug=Hs.309348 /len=487	AI475669	Hs.309348	
8709	0.032277	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
8710	0.00145	EST(cDNA clone IMAGE:6617359 5' )	BU569767		NP_005339
8715	0.023381	UI-H-DF0-bet-a-18-0-UI.s1 NCI_CGAP_DF0 cDNA clone UI-H-DF0-bet-a-18-0-UI 3', mRNA sequence /clone=UI-H-DF0-bet-a-18-0-UI /clone_end=3' /gb=BU617862 /gi=23284077 /ug=Hs.441168 /len=1092	BU617862	Hs.441168	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8720	0.024972	UI-H-EU0-azs-p-18-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE: 5853185 3', mRNA sequence /clone=IMAGE: 5853185 /clone_end=3' /gb=BQ183906 /gi=20359457 /ug=Hs.356538 /len=1068	BQ183906	Hs.356538	
8727	0.028428	Similar to L1 repeat, Tf subfamily, member. 14, clone IMAGE:4820809, mRNA /gb=BC030623 /gi=22539740 /ug=Hs.227591 /len=2185	BC030623	Hs.227591	
8754	0.028428	602072454F1 NCI_CGAP_Brn67 cDNA clone IMAGE:4215325 5', mRNA sequence /clone=IMAGE:4215325 /clone_end=5' /gb=BF530944 /gi=11618307 /ug=Hs.319823 /len=686	BF530944	Hs.319823	
8755	0.021876	UI-H-EI1-azd-l-09-0-UI.s1 NCI_CGAP_EI1 cDNA clone IMAGE:5847320 3', mRNA sequence /clone=IMAGE:5847320 /clone_end=3' /gb=BQ003406 /gi=19728306 /ug=Hs.269493 /len=1055	BQ003406	Hs.269493	
8757	0.00684	602319564F1 NIH_MGC_89 cDNA clone IMAGE:4415078 5', mRNA sequence /clone=IMAGE:4415078 /clone_end=5' /gb=BG249501 /gi=12759329 /ug=Hs.281067 /len=976	BG249501	Hs.281067	
8764	0.034358	mRNA; cDNA DKFZp761G241 (from clone DKFZp761G241) /gb=AL137501 /gi=6808146 /ug=Hs.306470 /len=3018	AL137501	Hs.306470	
8774	0.020453	EST(cDNA clone IMAGE:4257808 similar to contains Alu repetitive element; )	BG272788		
8777	0.030302	UI-E-EO1-ajc-l-12-0-UI.r1 UI-E-EO1 cDNA clone UI-E-EO1-ajc-l-12-0-UI 5', mRNA sequence /clone=UI-E-EO1-ajc-l-12-0-UI /clone_end=5' /gb=BM718946 /gi=19037365 /ug=Hs.364651 /len=1031	BM718946	Hs.364651	
8780	0.00299	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530	BF814502	Hs.446594	
8794	0.032277	AGENCOURT_8475922 Lupski_sympathetic_trunk cDNA clone IMAGE:6195208 5', mRNA sequence /clone=IMAGE:6195208 /clone_end=5' /gb=BQ721341 /gi=21860238 /ug=Hs.128076 /len=1186	BQ721341	Hs.128076	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8800	3.53E-04	UI-H-FH1-bfi-o-08-0-UI.s1 NCI_CGAP_FH1 cDNA clone UI-H-FH1-bfi-o-08-0-UI 3', mRNA sequence /clone=UI-H-FH1-bfi-o-08-0-UI /clone_end=3' /gb=CA427422 /gi=24790148 /ug=Hs.182545 /len=1150	CA427422	Hs.182545	
8826	0.043827	cDNA FLJ25058 fis, clone CBL04608. /cds=(139,639) /gb=AK057787 /gi=16553726 /ug=Hs.350624 /len=1808	AK057787	Hs.350624	
8827	0.020453	ob11d04.s1 NCI_CGAP_Kid3 cDNA clone IMAGE:1323367 3' similar to contains Alu repetitive element;contains element LTR5 repetitive element ;, mRNA sequence /clone=IMAGE:1323367 /clone_end=3' /gb=AA872730 /gi=2968852 /ug=Hs.125229 /len=586	AA872730	Hs.125229	
8836	0.026653	No significant match	SEQ.ID.No.33		
8863	0.036549	EST(cDNA clone IMAGE:290115 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ; )	N63269		
8865	0.01004	cDNA FLJ12091 fis, clone HEMBB1002582	AK022153		
8909	0.036549	WW domain-containing adapter with a coiled-coil region (WAC), transcript variant 2, mRNA /cds=(332,2140) /gb=NM_100264 /gi=18379329 /ug=Hs.70333 /len=3088	NM_100264	Hs.70333	NP_567823
8913	0.002294	EST xc94a04.x1 NCI_CGAP_Brn35 cDNA clone IMAGE:2591886 3' similar to contains element MSR1 repetitive element ;	AW090604		
8914	0.020596	EST (PM1-CT0247-101199-003-h12 CT0247	AW852630		
8946	0.014461	hypothetical protein FLJ33282 (FLJ33282), mRNA /cds=(225,1523) /gb=NM_152388 /gi=22748830 /ug=Hs.346509 /len=2078	NM_152388	Hs.346509	
8963	0.032277	EST(IL2-HT0433-020200-041-F07_1 HT0433)	BE161204		
8974	0.046501	BX094154 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998P17654, mRNA sequence /clone=IMAGp998P17654_/_IMAGE:293 632 /gb=BX094154 /gi=27826950 /ug=Hs.12962 /len=758	BX094154	Hs.12962	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8975	0.011644	7e58g12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:3286726 3', mRNA sequence /clone=IMAGE:3286726 /clone_end=3' /gb=BE644873 /gi=9969184 /ug=Hs.417404 /len=494	BE644873	Hs.417404	
8976	0.036549	wg12a04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:2364846 3', mRNA sequence /clone=IMAGE:2364846 /clone_end=3' /gb=AI800735 /gi=5366129 /ug=Hs.115122 /len=555	AI800735	Hs.115122	
9027	0.023381	UI-H-EU0-azt-n-21-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE: 5853524 3', mRNA sequence /clone=IMAGE: 5853524 /clone_end=3' /gb=BQ183977 /gi=20359528 /ug=Hs.421341 /len=1142	BQ183977	Hs.421341	
9029	0.020453	ol54a01.s1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1527240 3' similar to contains Alu repetitive element,, mRNA sequence /clone=IMAGE:1527240 /clone_end=3' /gb=AA917705 /gi=3057595 /ug=Hs.190264 /len=515	AA917705	Hs.190264	
9030	0.046501	EST(cDNA RC0-NT0113-300500-011- g05 NT0113)	BF366806		
9062	0.043827	qh54d02.x1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:1848483 3' similar to contains MER30.b3 MER30 repetitive element ;, mRNA sequence /clone=IMAGE:1848483 /clone_end=3' /gb=AI240813 /gi=3836210 /ug=Hs.368570 /len=459	AI240813	Hs.368570	
9080	0.032277	EST(cDNA clone IMAGE:4999711 5' )	BI092644		NP_004883
9101	0.036549	clone IMAGE:5261213, mRNA /gb=BC036485 /gi=22209057 /ug=Hs.26418 /len=2880	BC036485	Hs.26418	
9106	0.046501	yz39f06.s1 Morton Fetal Cochlea cDNA clone IMAGE:285443 3', mRNA sequence /clone=IMAGE:285443 /clone_end=3' /gb=N66393 /gi=1218518 /ug=Hs.102754 /len=618	N66393	Hs.102754	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9108	0.001747	UI-H-EI0-aye-c-17-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-aye-c-17-0-UI 3', mRNA sequence /clone=UI-H-EI0-aye-c-17-0-UI /clone_end=3' /gb=CA447385 /gi=24811805 /ug=Hs.420740 /len=812	CA447385	Hs.420740	
9129	0.021876	EST(cDNA.	AW896077		
9131	0.01004	ESTs, cDNA, 5' end /clone=IMAGE:4148900 /clone_end=5' /gb=BF342391 /gi=11289392 /ug=Hs.30469 /len=803	BF342391	Hs.30469	NP_055313
9137	0.034358	cDNA FLJ31919 fis, clone NT2RP7004964. /gb=AK056481 /gi=16551895 /ug=Hs.400872 /len=4013	AK056481	Hs.400872	
9147	0.046501	602507046F1 NIH_MGC_79 cDNA clone IMAGE:4604315 5', mRNA sequence /clone=IMAGE:4604315 /clone_end=5' /gb=BG435458 /gi=13341964 /ug=Hs.191168 /len=672	BG435458	Hs.191168	
9148	0.00684	DKFZp434M2216 (from clone DKFZp434M2216) /cds=UNKNOWN /gb=AL137295 /gi=6807756 /ug=Hs.199429 /len=1035	AL137295	Hs.199429	NP_004632
9153	0.015521	AGENCOURT_8584280 Lupski_sympathetic_trunk cDNA clone IMAGE:6192820 5', mRNA sequence /clone=IMAGE:6192820 /clone_end=5' /gb=BQ876563 /gi=22268571 /ug=Hs.346743 /len=925	BQ876563	Hs.346743	
9154	0.004205	mRNA; cDNA DKFZp564B213 (from clone DKFZp564B213) /gb=AL049240 /gi=4499973 /ug=Hs.380268 /len=767	AL049240	Hs.380268	
9155	0.034358	cDNA FLJ36544 fis, clone TRACH2006378. /gb=AK093863 /gi=21752807 /ug=Hs.101689 /len=2670	AK093863	Hs.101689	
9169	0.00326	EST(placenta Nb2HP cDNA clone IMAGE:132920 3' similar to contains Alu repetitive element;contains L1 repetitive element ;)	R25670		
9179	0.00632	UI-E-EJ1-ajf-o-07-0-UI.r1 UI-E-EJ1 cDNA clone UI-E-EJ1-ajf-o-07-0-UI 5', mRNA sequence /clone=UI-E-EJ1-ajf-o- 07-0-UI /clone_end=5' /gb=BM718282 /gi=19036470 /ug=Hs.439477 /len=1095	BM718282	Hs.439477	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9182	0.041279	os71f06.x1 NCI_CGAP_GC2 cDNA clone IMAGE:1610819 3', mRNA sequence /clone=IMAGE:1610819 /clone_end=3' /gb=AI082470 /gi=3419262 /ug=Hs.135463 /len=521	AI082470	Hs.135463	
9189	0.00632	clone IMAGE:5265581, mRNA /gb=BC035165 /gi=23272508 /ug=Hs.400548 /len=2237	BC035165	Hs.400548	
9190	0.017843	DKFZP564D116 protein (DKFZP564D116), mRNA /cds=(676,1965) /gb=NM_015631 /gi=24308108 /ug=Hs.181185 /len=2637	NM_015631	Hs.181185	NP_056446
9230	0.01911	hn49c02.x1 NCI_CGAP_Co17 cDNA clone IMAGE:3026978 3' similar to contains MER5.b1 MER5 repetitive element ;, mRNA sequence /clone=IMAGE:3026978 /clone_end=3' /gb=AW770800 /gi=7702847 /ug=Hs.371969 /len=463	AW770800	Hs.371969	
9232	0.011644	clone IMAGE:5265853, mRNA /gb=BC037736 /gi=23337068 /ug=Hs.397840 /len=3811	BC037736	Hs.397840	
9235	3.53E-04	cDNA FLJ13558 fis, clone PLACE1007743. /gb=AK023620 /gi=10435601 /ug=Hs.86043 /len=2271	AK023620	Hs.86043	
9243	0.043827	AV700621 GKC cDNA clone GKCDKF09 3', mRNA sequence /clone=GKCDKF09 /clone_end=3' /gb=AV700621 /gi=10302592 /ug=Hs.191445 /len=809	AV700621	Hs.191445	
9259	0.016648	th92f12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:2126159 3' similar to SW:DOC2_MOUSE P98078 MITOGEN-RESPONSIVE PHOSPHOPROTEIN ISOFORMS P96, P93 AND P67. ;, mRNA sequence /clone=IMAGE:2126159 /clone_end=3' /gb=AI435504 /gi=4303646 /ug=Hs.443955 /len=545	AI435504	Hs.443955	
9266	0.005382	clone FLB2932 mRNA sequence /gb=AF138859 /gi=7340965 /ug=Hs.274405 /len=2990	AF138859	Hs.274405	
9270	0.028428	602122561F1 NIH_MGC_56 cDNA clone IMAGE:4279766 5', mRNA sequence /clone=IMAGE:4279766 /clone_end=5' /gb=BF668349 /gi=11942244 /ug=Hs.44731 /len=906	BF668349	Hs.44731	
9281	0.015521	EST(cDNA clone MDSDHE04 5' )	AV759672		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9298	0.021876	ad47h05.s1 Stratagene lung carcinoma 937218 cDNA clone IMAGE:884889 3' similar to gb:X51956_rna1 GAMMA ENOLASE Alu repetitive element;contains element TAR1 repetitive element ;, mRNA sequence /clone=IMAGE:884889 /clone_end=3' /gb=AA669458 /gi=2630957 /ug=Hs.445542 /len=926	AA669458	Hs.445542	
9318	0.002294	No significant match	SEQ.ID.No.102		
9327	0.009313	EST, mRNA; cDNA DKFZp566M063 (from clone DKFZp566M063)	AL110194		NP_002119
9350	0.028428	No significant match, ORF+2(389~530)	SEQ.ID.No.87		
9351	0.004569	No significant match, ORF+3(126~266)	SEQ.ID.No.91		
9354	0.017843	No significant match (ORF:- 3:151~300[150])	SEQ.ID.No.60		
9369	0.049308	UI-E-EJ0-ahj-l-23-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahj-l-23-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahj-l-23-0-UI /clone_end=5' /gb=BM701102 /gi=19014360 /ug=Hs.63236 /len=1511	BM701102	Hs.63236	
9390	0.021876	ribosomal protein L13a (RPL13A), mRNA /cds=(23,634) /gb=NM_012423 /gi=14591905 /ug=Hs.389335 /len=1142	NM_012423	Hs.389335	NP_036555
9392	0.00274	AGENCOURT_6400386 NIH_MGC_67 cDNA clone IMAGE:5495662 5', mRNA sequence /clone=IMAGE:5495662 /clone_end=5' /gb=BM799714 /gi=19116537 /ug=Hs.356635 /len=1153	BM799714	Hs.356635	
9427	0.023381	Enah/Vasp-like (EVL), mRNA /cds=(62,1318) /gb=NM_016337 /gi=7706686 /ug=Hs.241471 /len=1833	NM_016337	Hs.241471	NP_057421
9459	0.041279	ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=NM_006294 /gi=20070231 /ug=Hs.131255 /len=965	NM_006294	Hs.131255	NP_006285
9466	0.030302	hypothetical protein FLJ10891 (FLJ10891), mRNA /cds=(128,1525) /gb=NM_018260 /gi=8922743 /ug=Hs.274169 /len=2864	NM_018260	Hs.274169	NP_060730
9475	0.001915	hypothetical protein FLJ20624 (FLJ20624), mRNA /cds=(80,1255) /gb=NM_017906 /gi=8923576 /ug=Hs.52256 /len=1554	NM_017906	Hs.52256	NP_060376
9497	0.028428	myotubularin related protein 9 (MTMR9), mRNA /cds=(83,1732) /gb=NM_015458 /gi=19923423 /ug=Hs.48802 /len=7081	NM_015458	Hs.48802	NP_056273

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9508	0.023381	similar to RIKEN cDNA 1810055D05 (LOC131118), mRNA /cds=(125,475) /gb=NM_145261 /gi=21687101 /ug=Hs.349177 /len=580	NM_145261	Hs.349177	NP_660304
9526	0.020453	C6orf37 mRNA, complete cds /cds=(294,1607) /gb=AF350451 /gi=21427109 /ug=Hs.10784 /len=5571	AF350451	Hs.10784	NP_060103
9589	0.021876	abhydrolase domain containing 3 (ABHD3), mRNA /cds=(110,1339) /gb=NM_138340 /gi=23397662 /ug=Hs.13377 /len=2049	NM_138340	Hs.13377	NP_612213
9590	0.024972	cDNA FLJ30977 fis, clone HHDP2000095, highly similar to Cricetulus griseus layilin mRNA. /cds=(338,1462) /gb=AK055539 /gi=16550287 /ug=Hs.133015 /len=2067	AK055539	Hs.133015	NP_849156
9596	0.049308	vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851	NM_003380	Hs.297753	NP_000995
9617	0.030302	mRNA; cDNA DKFZp761B0823 (from clone DKFZp761B0823) /gb=AL157462 /gi=7018477 /ug=Hs.306484 /len=5085	AL157462	Hs.306484	
9632	0.005835	clone MGC:9947 IMAGE:3876105, mRNA, complete cds /cds=(51,2216) /gb=BC013590 /gi=15488925 /ug=Hs.2437 /len=2651	BC013590	Hs.2437	
9665	0.041279	EST(df64h05.y1 Morton Fetal Cochlea clone IMAGE:2488569 5') (5e-06 match)	AW024055		
9684	0.043827	cDNA FLJ40989 fis, clone UTERU2015108. /gb=AK098308 /gi=21758297 /ug=Hs.325568 /len=2316	AK098308	Hs.325568	
9712	0.008631	wl54c05.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2428712 3', mRNA sequence /clone=IMAGE:2428712 /clone_end=3' /gb=AI864553 /gi=5528660 /ug=Hs.371597 /len=474	AI864553	Hs.371597	
9728	0.030302	EST(ow54e12.s1 Soares_parathyroid_tumor_NbHPA clone IMAGE:1650670 3')	AI022887		
9730	0.014461	601862578F1 NIH_MGC_53 cDNA clone IMAGE:4082082 5', mRNA sequence /clone=IMAGE:4082082 /clone_end=5' /gb=BF207870 /gi=11101456 /ug=Hs.396179 /len=756	BF207870	Hs.396179	
9736	0.00684	EST(wl38a07.x1 NCI_CGAP_Ut1 clone IMAGE:2427156 3')	AI858415		NP_079457



Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9758	0.004205	UI-E-DX0-agr-j-18-0-UI.s1 UI-E-DX0 cDNA clone UI-E-DX0-agr-j-18-0-UI 3', mRNA sequence /clone=UI-E-DX0-agr-j-18-0-UI /clone_end=3' /gb=BM667357 /gi=18975188 /ug=Hs.436172 /len=983	BM667357	Hs.436172	
9774	0.021876	cDNA FLJ36605 fis, clone TRACH2015316, highly similar to VIMENTIN. /cds=(631,1317) /gb=AK093924 /gi=21752883 /ug=Hs.379100 /len=2665	AK093924	Hs.379100	
9784	0.043827	CocoaCrisp (LOC83690), mRNA /cds=(376,1878) /gb=NM_031461 /gi=21314740 /ug=Hs.182364 /len=2962	NM_031461	Hs.182364	NP_113649
9796	0.038855	mRNA; cDNA DKFZp564C2063 (from clone DKFZp564C2063) /gb=AL117595 /gi=5912159 /ug=Hs.4055 /len=1444	AL117595	Hs.4055	
9814	0.010816	clone MGC:20208 IMAGE:3936339, mRNA, complete cds /cds=(330,1832) /gb=BC014000 /gi=15559281 /ug=Hs.58461 /len=2733	BC014000	Hs.58461	
9830	0.001592	mRNA for KIAA0219 gene, partial cds. /cds=(1,8029) /gb=D86973 /gi=20521847 /ug=Hs.75354 /len=8608	D86973	Hs.75354	
9833	0.01911	AGENCOURT_6861057 NIH_MGC_99 cDNA clone IMAGE:5931113 5', mRNA sequence /clone=IMAGE:5931113 /clone_end=5' /gb=BQ066467 /gi=19895513 /ug=Hs.446485 /len=1029	BQ066467	Hs.446485	
9855	0.013463	potent brain type organic ion transporter (BOCT), transcript variant 1, mRNA /cds=(57,1673) /gb=NM_020372 /gi=21361833 /ug=Hs.373498 /len=2090	NM_020372	Hs.373498	NP_065105
9869	0.00145	Nedd4 family interacting protein 1 (NDFIP1), mRNA /cds=(105,770) /gb=NM_030571 /gi=13386479 /ug=Hs.9788 /len=1837	NM_030571	Hs.9788	NP_085048
9891	0.021876	isocitrate dehydrogenase 2 (NADP ), mitochondrial (IDH2), nuclear gene encoding mitochondrial protein, mRNA /cds=(87,1445) /gb=NM_002168 /gi=28178831 /ug=Hs.5337 /len=1740	NM_002168	Hs.5337	NP_002159
9907	0.020453	glucuronidase, beta (GUSB), mRNA /cds=(27,1982) /gb=NM_000181 /gi=4504222 /ug=Hs.183868 /len=2191	NM_000181	Hs.183868	NP_000172
9909	0.021876	clone IMAGE:5263531, mRNA /gb=BC037740 /gi=22902216 /ug=Hs.18016 /len=5036	BC037740	Hs.18016	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9911	0.007397	DKFZP586A0522 protein (DKFZP586A0522), mRNA /cds=(21,755) /gb=NM_014033 /gi=13378140 /ug=Hs.288771 /len=1705	NM_014033	Hs.288771	NP_054752
9918	0.023381	chromosome 20 open reading frame 108 (C20orf108), mRNA /cds=(41,619) /gb=NM_080821 /gi=18201877 /ug=Hs.352413 /len=3026	NM_080821	Hs.352413	NP_543011
9934	0.020453	aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA /cds=(21,2363) /gb=NM_001098 /gi=4501866 /ug=Hs.300463 /len=2467	NM_001098	Hs.300463	NP_001089
9953	0.026653	Fatty acid binding protein 1, liver (Fabp1), mRNA	NM_012556		
9960	0.005835	similar to weakly similar to glutathione peroxidase 2, clone MGC:32677 IMAGE:4285958, mRNA, complete cds /cds=(35,664) /gb=BC029424 /gi=20810222 /ug=Hs.283072 /len=1398	BC029424	Hs.283072	
9972	0.032277	caldesmon 1 (CALD1), transcript variant 1, mRNA /cds=(230,2611) /gb=NM_033138 /gi=15149460 /ug=Hs.325474 /len=3610	NM_033138	Hs.325474	NP_149347
9982	0.017843	ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA /cds=(71,1603) /gb=NM_020038 /gi=9955973 /ug=Hs.90786 /len=5380	NM_020038	Hs.90786	NP_064422
10026	0.01004	dishevelled associated activator of morphogenesis 1 (DAAM1), mRNA /cds=(126,3362) /gb=NM_014992 /gi=21071076 /ug=Hs.197751 /len=4256	NM_014992	Hs.197751	NP_055807
10039	0.038855	keratinocytes associated protein 2 (KCP2), mRNA /cds=(1,489) /gb=NM_173852 /gi=27777660 /ug=Hs.374854 /len=489	NM_173852	Hs.374854	NP_776251
10064	0.041279	KIAA0570 gene product (KIAA0570), mRNA	XM_002692		
10095	0.026653	O-sialoglycoprotein endopeptidase (OSGEP), mRNA /cds=(130,1137) /gb=NM_017807 /gi=8923379 /ug=Hs.108894 /len=1394	NM_017807	Hs.108894	NP_060277
10101	0.032277	similar to G-protein gamma-12 subunit (LOC94680), mRNA	XM_040593		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10102	0.023381	hypothetical protein FLJ23445 (FLJ23445), mRNA /cds=(44,658) /gb=NM_025075 /gi=13376622 /ug=Hs.288151 /len=963	NM_025075	Hs.288151	NP_079351
10116	0.024972	splicing factor 1 (SF1), mRNA /cds=(383,2254) /gb=NM_004630 /gi=4759339 /ug=Hs.180677 /len=3131	NM_004630	Hs.180677	NP_004621
10134	0.01911	xl59d02.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2678979 3', mRNA sequence /clone=IMAGE:2678979 /clone_end=3' /gb=AW190111 /gi=6464591 /ug=Hs.377837 /len=248	AW190111	Hs.377837	
10148	0.043827	EST(qo26g10.x1 NCI_CGAP_Lu5 clone IMAGE:1909698 3' contains Alu repeat)	AI342863		
10170	0.043827	EST (ts95a10.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2239002 3')	AI635513		
10179	0.00684	EST (wq27e08.x1 NCI_CGAP_Kid11 IMAGE:2472518 3')	AI953360		NP_620149
10196	0.038855	UI-CF-DU1-aav-k-08-0-UI.s1 UI-CF-DU1 cDNA clone UI-CF-DU1-aav-k-08-0-UI 3', mRNA sequence /clone=UI-CF-DU1-aav-k-08-0-UI /clone_end=3', /gb=BM983293 /gi=19607660 /ug=Hs.424609 /len=684	BM983293	Hs.424609	
10217	0.028428	EST (wi53c12.x1 NCI_CGAP_Co16 cDNA clone IMAGE:2393974 3')	AI762075		NP_002884
10226	0.043827	wm98f08.x1 NCI_CGAP_Ut2 cDNA clone IMAGE:2444007 3' similar to contains Alu repetitive element;contains element MIR repetitive element ;, mRNA sequence /clone=IMAGE:2444007 /clone_end=3' /gb=AI889396 /gi=5594560 /ug=Hs.212245 /len=434	AI889396	Hs.212245	
10236	0.043827	hypothetical protein MGC4701 (MGC4701), mRNA /cds=(149,1585) /gb=NM_024511 /gi=24308290 /ug=Hs.421054 /len=1686	NM_024511	Hs.421054	NP_078787
10247	0.013463	vimentin (VIM) gene	M18895		
10276	0.043827	Hypothetical protein(cDNA sequence FLJ11311 fis, clone PLACE1010102) (=cDNA sequence DKFZp566J2146)	AK002173		NP_689971
10277	0.00274	likely ortholog of mouse embryonic epithelial gene 1 (EEG1), mRNA /cds=(319,1794) /gb=NM_017611 /gi=18252046 /ug=Hs.274453 /len=2630	NM_017611	Hs.274453	NP_060081
10282	0.041279	EST (7o83a06.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:3642898 3')	BF197462		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10283	0.041279	EST xs47d05.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2772777 3'	AW269335		NP_476500
10286	0.007397	Similar to cell death activator CIDE-3, clone MGC:50748 IMAGE:5204770, mRNA, complete cds /cds=(432,617) /gb=BC043599 /gi=27694390 /ug=Hs.432698 /len=1832	BC043599	Hs.432698	
10289	0.024972	EST RC3-HT0593-170300-011-c10 HT0593	BE177303		
10304	0.028428	cDNA FLJ14175 fis, clone NT2RP2002979. /gb=AK024237 /gi=10436564 /ug=Hs.288613 /len=3493	AK024237	Hs.288613	
10307	0.034358	EST(ti95f04.x1 NCI_CGAP_Gas4 cDNA clone IMAGE:2139775 3')	AI445690		
10315	0.030302	EST ( MR0-HT0407-010200-008-g12 HT0407	BE159321		
10346	0.021876	UI-E-EO1-aiv-e-19-0-UI.s1 UI-E-EO1 cDNA clone UI-E-EO1-aiv-e-19-0-UI 3', mRNA sequence /clone=UI-E-EO1-aiv-e-19-0-UI /clone_end=3' /gb=BU742864 /gi=23689787 /ug=Hs.356716 /len=1044	BU742864	Hs.356716	
10347	0.038855	hypothetical protein dJ122O8.2 (DJ122O8.2), mRNA /cds=(34,300) /gb=NM_020466 /gi=20070310 /ug=Hs.268115 /len=902	NM_020466	Hs.268115	NP_065199
10364	0.005382	EST (QV3-NN1023-130500-178-g10 NN1023)	AW902437		
10379	0.041279	EST (tc71e05.x1 Soares_NhHMPu_S1 cDNA clone IMAGE:2070080 3')	AI804457		NP_002067
10386	0.00274	UI-H-BW0-ajj-h-09-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2732033 3', mRNA sequence /clone=IMAGE:2732033 /clone_end=3' /gb=AW298400 /gi=6704960 /ug=Hs.438172 /len=635	AW298400	Hs.438172	
10408	0.044761	yr31a03.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:206860 5' similar to contains MER19 repetitive element ;, mRNA sequence /clone=IMAGE:206860 /clone_end=5' /gb=R98895 /gi=985496 /ug=Hs.125823 /len=377	R98895	Hs.125823	
10418	0.049308	602152595F1 NIH_MGC_81 cDNA clone IMAGE:4293719 5', mRNA sequence /clone=IMAGE:4293719 /clone_end=5' /gb=BF672139 /gi=11946034 /ug=Hs.19479 /len=896	BF672139	Hs.19479	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10471	0.012525	hypothetical protein FLJ14596 (FLJ14596), mRNA /cds=(1324,1968) /gb=NM_032809 /gi=19923651 /ug=Hs.325309 /len=3597	NM_032809	Hs.325309	NP_116198
10482	0.046501	EST(cDNA clone IMAGE:4588661 5')	BG422853		
10498	0.044761	wo45d05.x1 NCI_CGAP_Gas4 cDNA clone IMAGE:2458281 3' similar to contains element XTR repetitive element ;, mRNA sequence /clone=IMAGE:2458281 /clone_end=3' /gb=AI926493 /gi=5662457 /ug=Hs.213840 /len=509	AI926493	Hs.213840	
10504	0.003866	AGENCOURT_8152128 Lupski_dorsal_root_ganglion cDNA clone IMAGE:6184005 5', mRNA sequence /clone=IMAGE:6184005 /clone_end=5' /gb=BU145410 /gi=22658942 /ug=Hs.304440 /len=889	BU145410	Hs.304440	
10529	0.026653	df27e02.w1 Morton Fetal Cochlea cDNA clone IMAGE:2484578 3', mRNA sequence /clone=IMAGE:2484578 /clone_end=3' /gb=BI492664 /gi=15332008 /ug=Hs.345490 /len=657	BI492664	Hs.345490	
10531	0.020453	mRNA; cDNA DKFZp686J172 (from clone DKFZp686J172) /gb=AL832206 /gi=21732751 /ug=Hs.56896 /len=6055	AL832206	Hs.56896	
10536	0.037211	nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916 /len=797	NM_005594	Hs.32916	NP_005585
10539	0.024972	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
10551	0.003552	EST(cDNA clone IMAGE:814978 3' similar to TR:E91737 E91737 REVERSE TRANSCRIPTASE HOMOLOG {L1 REPETITIVE ELEMENT} ;contains L1.t1 L1 repetitive element ; )	AA465709		
10558	0.017843	ESTs, cDNA /clone=IMAGE:1372579 /gb=AA833868 /gi=2908636 /ug=Hs.156300 /len=495	AA833868	Hs.156300	
10559	0.019111	UI-E-CL1-afg-c-18-0-UI.r1 UI-E-CL1 cDNA clone UI-E-CL1-afg-c-18-0-UI 5', mRNA sequence /clone=UI-E-CL1-afg-c-18-0-UI /clone_end=5' /gb=BM691757 /gi=19005015 /ug=Hs.11355 /len=1234	BM691757	Hs.11355	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10561	0.017843	wn03h10.x1 NCI_CGAP_Ut2 cDNA clone IMAGE:2444419 3', mRNA sequence /clone=IMAGE:2444419 /clone_end=3' /gb=AI924266 /gi=5660230 /ug=Hs.370113 /len=514	AI924266	Hs.370113	
10583	0.030746	AV700930 GKC cDNA clone GKCBRB12 3', mRNA sequence /clone=GKCBRB12 /clone_end=3' /gb=AV700930 /gi=10302901 /ug=Hs.285894 /len=746	AV700930	Hs.285894	
10593	0.017843	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693	NM_020648	Hs.247302	NP_065699
10623	0.009313	clone IMAGE:5276765, mRNA /cds=UNKNOWN /gb=BC031314 /gi=21410747 /ug=Hs.26766 /len=1000	BC031314	Hs.26766	
10624	0.021876	AGENCOURT_6417307 NIH_MGC_67 cDNA clone IMAGE:5492062 5', mRNA sequence /clone=IMAGE:5492062 /clone_end=5' /gb=BM799896 /gi=19116719 /ug=Hs.304926 /len=913	BM799896	Hs.304926	
10629	0.049308	ac74b05.x5 Stratagene lung (#937210) cDNA clone IMAGE:868305 3' similar to contains Alu repetitive element, mRNA sequence /clone=IMAGE:868305 /clone_end=3' /gb=AI791153 /gi=5338869 /ug=Hs.444952 /len=498	AI791153	Hs.444952	
10636	0.007397	cDNA FLJ13571 fis, clone PLACE1008405. /gb=AK023633 /gi=10435617 /ug=Hs.116278 /len=2484	AK023633	Hs.116278	
10644	0.021876	EST(cDNA clone GKCEND03 5' )	AV683165		
10657	0.028428	cDNA FLJ34771 fis, clone NT2NE2003150. /gb=AK092090 /gi=21750599 /ug=Hs.433010 /len=2424	AK092090	Hs.433010	
10658	0.012525	hypothetical protein MGC10233 (MGC10233), mRNA /cds=(547,1389) /gb=NM_152715 /gi=22749416 /ug=Hs.29041 /len=3915	NM_152715	Hs.29041	NP_689928
10661	0.013463	ip18c02.y1 HR85 islet cDNA clone IMAGE:6217706 5', mRNA sequence /clone=IMAGE:6217706 /clone_end=5' /gb=CA777576 /gi=26015451 /ug=Hs.115779 /len=700	CA777576	Hs.115779	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10666	0.017843	EST384170 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW971961 /gi=8161927 /ug=Hs.136340 /len=642	AW971961	Hs.136340	
10705	0.015521	No significant match, ORF+2(386~529),+3(3~107)	SEQ.ID.No.2		
10729	0.01911	myc-induced nuclear antigen, 53 kDa (MINA53), transcript variant 2, mRNA /cds=(214,1608) /gb=NM_032778 /gi=23346417 /ug=Hs.23294 /len=2221	NM_032778	Hs.23294	NP_116167
10732	0.046501	EST(Kawakami zebrafish DRA Danio rerio cDNA clone 2640570 3')	AW343514		
10746	0.017843	No significant match (ORF:+3:69~302[234])	SEQ.ID.No.27		
10765	0.024972	EST oy92c03.x1 Soares_fetal_liver_spleen_1NFLS_S1 H.sapiens cDNA clone IMAGE:1673284 3'	AI076100		
10773	0.026653	EST (RC3-CT0254-300800-022-g07 CT0254)	BE927223		
10777	0.01911	EST (wm51f05.x1 NCI_CGAP_Ut2 IMAGE:2439489 3')	AI871724		
10779	0.049308	EST (ADB cDNA clone ADBAKA02 5')	AV704531		
10782	0.023381	EST (cDNA clone IMAGE:120476 3' similar to	T95469		
10786	0.021876	EST (MR0-SN0040-060400-001-h09 SN0040)	AW867719		
10798	0.026653	EST (ta16g05.x1 NCI_CGAP_Lym5 IMAGE:2044280 3')	AI471814		
10799	0.026653	cDNA FLJ11934 fis, clone HEMBB1000510. /gb=AK021996 /gi=10433305 /ug=Hs.261699 /len=2599	AK021996	Hs.261699	
10805	0.032277	EST(ak84d11.s1 Barstead spleen HPLRB2 cDNA clone IMAGE:1414581 3' similar to contains MER10.t3 MER10 repetitive element)	AA845289		
10817	0.016648	EST(hz33h07.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3209821 3')	BE504880		
10842	0.020453	EST (nc45b12.s1 NCI_CGAP_Pr3 cDNA clone IMAGE:1011071 similar to contains Alu repetitive element)	AA229160		
10847	0.005835	hypothetical protein MGC3200 (MGC3200), mRNA /cds=(108,764) /gb=NM_032305 /gi=14150063 /ug=Hs.9088 /len=1191	NM_032305	Hs.9088	NP_115681
10860	0.009313	mitochondrion, complete genome	NC_001807		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10861	0.032277	UI-CF-EC1-aea-g-11-0-UI.s1 UI-CF-EC1 cDNA clone UI-CF-EC1-aea-g-11-0-UI 3', mRNA sequence /clone=UI-CF-EC1-aea-g-11-0-UI /clone_end=3' /gb=BU688263 /gi=23544886 /ug=Hs.336400 /len=528	BU688263	Hs.336400	
10863	0.002294	EST(TCBAP1E0695 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA clone TCBAP0695)	BE243837		NP_006241
10888	0.034358	UI-H-DH0-aui-j-10-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871081 3', mRNA sequence /clone=IMAGE:5871081 /clone_end=3' /gb=BM994461 /gi=19719362 /ug=Hs.434057 /len=2059	BM994461	Hs.434057	
10899	0.007397	ad44d12.x5 Stratagene lung carcinoma 937218 cDNA clone IMAGE:884567 3' similar to contains Alu repetitive element;contains L1.t1 L1 repetitive element ;, mRNA sequence /clone=IMAGE:884567 /clone_end=3' /gb=AI732123 /gi=5053258 /ug=Hs.446065 /len=484	AI732123	Hs.446065	
10909	0.017843	EST (MR1-SN0062-100500-002-g03 SN0062 cDNA)	AW868480		
10926	0.015521	EST(y57a07.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:191508 3' similar to gb:X56411_rna1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN)	H37798		
10937	0.024972	hypothetical protein MGC16384 (MGC16384), mRNA /cds=(450,602) /gb=NM_053048 /gi=16596689 /ug=Hs.274268 /len=1599	NM_053048	Hs.274268	NP_444276
10940	0.034358	mRNA; cDNA DKFZp686K192 (from clone DKFZp686K192) /gb=AL832209 /gi=21732754 /ug=Hs.259347 /len=6707	AL832209	Hs.259347	
10943	0.017843	mRNA; cDNA DKFZp547K0918 (from clone DKFZp547K0918) /gb=AL832566 /gi=21733141 /ug=Hs.271324 /len=1883	AL832566	Hs.271324	
10947	0.041279	ESTs, cDNA /gb=AW959468 /gi=8149152 /ug=Hs.188738 /len=767	AW959468	Hs.188738	
10950	0.023381	cDNA FLJ38913 fis, clone NT2NE2008017. /gb=AK096232 /gi=21755673 /ug=Hs.50094 /len=2555	AK096232	Hs.50094	NP_835224



Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10958	0.028428	FLJ30424 fis, clone BRACE2008881, weakly similar to ZINC FINGER PROTEIN 195 /cds=UNKNOWN /gb=AK054986 /gi=16549625 /ug=Hs.21423 /len=2144	AK054986	Hs.21423	
10969	0.01911	cDNA FLJ37747 fis, clone BRHIP2022986. /gb=AK095066 /gi=21754256 /ug=Hs.289068 /len=3097	AK095066	Hs.289068	
10979	0.00145	mRNA full length insert cDNA clone EUROIMAGE 1913076. /gb=AL359062 /gi=8518189 /ug=Hs.41271 /len=1779	AL359062	Hs.41271	
10989	0.011644	BX102645 NCI_CGAP_Brn23 cDNA clone IMAGp998L144327, mRNA sequence /clone=IMAGp998L144327 IMAGE:1703965 /gb=BX102645 /gi=27831887 /ug=Hs.146883 /len=786	BX102645	Hs.146883	
11002	0.024972	AU119153 HEMBA1 cDNA clone HEMBA1005152 5', mRNA sequence /clone=HEMBA1005152 /clone_end=5' /gb=AU119153 /gi=10934388 /ug=Hs.288615 /len=820	AU119153	Hs.288615	
11004	0.00684	Similar to UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase 9 (GalNAc-T9), clone MGC:43305 IMAGE:5265475, mRNA, complete cds /cds=(416,2239) /gb=BC037341 /gi=22713621 /ug=Hs.351204 /len=2525	BC037341	Hs.351204	
11025	0.004961	EST(cDNA 3'	BM264491		
11046	0.009313	wc25f11.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2316237 3', mRNA sequence /clone=IMAGE:2316237 /clone_end=3' /gb=AI678258 /gi=4888440 /ug=Hs.174257 /len=585	AI678258	Hs.174257	
11052	0.005382	cDNA FLJ40815 fis, clone TRACH2010600. /gb=AK098134 /gi=21758081 /ug=Hs.432620 /len=2814	AK098134	Hs.432620	
11057	0.011644	7l80c03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:3527788 3' similar to TR:O88246 O88246 MSZF14 ;, mRNA sequence /clone=IMAGE:3527788 /clone_end=3' /gb=BF196920 /gi=11085469 /ug=Hs.419997 /len=511	BF196920	Hs.419997	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11061	0.015521	clone IMAGE:3887266, mRNA /gb=BC015512 /gi=15930151 /ug=Hs.88013 /len=1505	BC015512	Hs.88013	
11063	0.017843	clone alpha_est218/52C1 mRNA sequence /gb=AF001542 /gi=2529714 /ug=Hs.356442 /len=2992	AF001542	Hs.356442	
11081	0.003551	cDNA /clone=IMAGE:997623 /gb=AA533447 /gi=2277543 /ug=Hs.312989 /len=474	AA533447	Hs.312989	NP_000601
11082	0.014461	UI-1-BB1p-avc-e-03-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-avc-e-03-0-UI 3', mRNA sequence /clone=UI-1-BB1p-avc-e-03-0-UI /clone_end=3' /gb=BU754312 /gi=23713100 /ug=Hs.355575 /len=1086	BU754312	Hs.355575	
11083	0.032277	EST(cDNA clone IMAGE:2675214 3')	AW189289		NP_001116
11090	0.007994	UI-H-FT1-bhv-c-13-0-UI.s1 NCI_CGAP_FT1 cDNA clone UI-H-FT1-bhv-c-13-0-UI 3', mRNA sequence /clone=UI-H-FT1-bhv-c-13-0-UI /clone_end=3' /gb=CA748480 /gi=25568160 /ug=Hs.22883 /len=1102	CA748480	Hs.22883	
11116	0.016648	cDNA FLJ33668 fis, clone BRAMY2028565. /gb=AK090987 /gi=21749256 /ug=Hs.346796 /len=2294	AK090987	Hs.346796	
11125	0.049308	EST(cDNA clone IMAGE:2815110 3')	AW268719		
11126	0.012525	full length insert cDNA clone ZD64C04 /gb=AF088052 /gi=3523258 /ug=Hs.384557 /len=831	AF088052	Hs.384557	
11192	0.01911	RC4-HT0277-160200-013-d07 HT0277 cDNA, mRNA sequence /gb=BE151126 /gi=8613847 /ug=Hs.158600 /len=571	BE151126	Hs.158600	
11202	0.01911	AV699513 GKC cDNA clone GKCDLA08 3', mRNA sequence /clone=GKCDLA08 /clone_end=3' /gb=AV699513 /gi=10301484 /ug=Hs.131366 /len=793	AV699513	Hs.131366	
11215	0.003866	Novel, ORF+3(39~203)	SEQ.ID.No.53		
11253	0.012525	hypothetical protein similar to beta-transducin family (FLJ10458), mRNA /cds=(14,1471) /gb=NM_018096 /gi=20070287 /ug=Hs.85570 /len=2593	NM_018096	Hs.85570	NP_060566
11295	0.013463	collagen, type V, alpha 1 (COL5A1), mRNA /cds=(383,5899) /gb=NM_000093 /gi=16554578 /ug=Hs.146428 /len=6496	NM_000093	Hs.146428	NP_000084

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11303	0.00632	S100 calcium binding protein A1 (S100A1), mRNA /cds=(114,398) /gb=NM_006271 /gi=5454031 /ug=Hs.433503 /len=607	NM_006271	Hs.433503	NP_006262
11316	0.026979	KIAA1721 protein, partial cds /cds=UNKNOWN /gb=AB051508 /gi=12697986 /ug=Hs.117102 /len=8047	AB051508	Hs.117102	NP_071904
11318	0.016693	SAR1 protein (SAR1), mRNA /cds=(125,721) /gb=NM_020150 /gi=21361614 /ug=Hs.110796 /len=3003	NM_020150	Hs.110796	
11335	0.012525	COX11 cytochrome c oxidase assembly protein (yeast) (COX11), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,878) /gb=NM_004375 /gi=17921983 /ug=Hs.241515 /len=2717	NM_004375	Hs.241515	NP_004366
11339	0.026653	hypothetical protein FLJ20986 (FLJ20986), mRNA /cds=(1758,3863) /gb=NM_024524 /gi=21362055 /ug=Hs.324507 /len=5226	NM_024524	Hs.324507	NP_078800
11379	0.007994	hypothetical protein FLJ20038 (FLJ20038), mRNA /cds=(274,720) /gb=NM_017634 /gi=8923043 /ug=Hs.72071 /len=2571	NM_017634	Hs.72071	NP_060104
11383	0.023381	DKFZP586G011 protein (LAP1B), mRNA /cds=(56,1444) /gb=NM_015602 /gi=24308098 /ug=Hs.234265 /len=3275	NM_015602	Hs.234265	NP_056417
11387	0.049308	df22c07.w1 Morton Fetal Cochlea cDNA clone IMAGE:2484085 3', mRNA sequence /clone=IMAGE:2484085 /clone_end=3' /gb=BI492292 /gi=15331636 /ug=Hs.379172 /len=359	BI492292	Hs.379172	
11397	0.038855	Niemann-Pick disease, type C2 (NPC2), mRNA /cds=(116,571) /gb=NM_006432 /gi=20149580 /ug=Hs.433222 /len=929	NM_006432	Hs.433222	NP_006423
11399	0.016648	density-regulated protein (DENR), mRNA /cds=(111,707) /gb=NM_003677 /gi=27501445 /ug=Hs.22393 /len=2766	NM_003677	Hs.22393	NP_003668
11401	0.01911	hypothetical protein PRO1843 (PRO1843), mRNA /cds=(965,1255) /gb=NM_018507 /gi=8924082 /ug=Hs.283330 /len=1268	NM_018507	Hs.283330	NP_060977

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11407	0.023381	Similar to proline synthetase co-transcribed (bacterial homolog), clone MGC:2667 IMAGE:3546307, mRNA, complete cds /cds=(67,894) /gb=BC012334 /gi=15147390 /ug=Hs.301959 /len=2580	BC012334	Hs.301959	NP_009129
11537	8.10E-04	UI-H-DF1-auf-c-04-0-UI.s1 NCI_CGAP_DF1 cDNA clone IMAGE:5868603 3', mRNA sequence /clone=IMAGE:5868603 /clone_end=3' /gb=BM992029 /gi=19711418 /ug=Hs.358825 /len=1052	BM992029	Hs.358825	
11539	0.017843	mRNA for KIAA1327 protein, partial cds. /cds=(1,5417) /gb=AB037748 /gi=20521883 /ug=Hs.106204 /len=6687	AB037748	Hs.106204	
11554	0.038855	EST(df27f12.y1 Morton Fetal Cochlea clone IMAGE:2484646 5')	AW021741		NP_057485
11576	0.041279	EST(CM4-ST0276-101299-059-d05 ST0276)	AW392874		
11582	7.33E-04	RC1-NN0073-090500-012-f02 NN0073 cDNA, mRNA sequence /gb=AW898615 /gi=8062820 /ug=Hs.130729 /len=660	AW898615	Hs.130729	
11585	0.041279	EST (yd08e03.r1 clone 24895 5')	T80443		
11596	0.028428	hypothetical protein cDNA DKFZp761K1115 (from clone DKFZp761K1115); partial cds	AL162046		NP_060717
11598	0.036549	adenylate kinase 3 like 1 (AK3L1), mRNA /cds=(141,824) /gb=NM_016282 /gi=19923436 /ug=Hs.43436 /len=2642	NM_016282	Hs.43436	NP_057366
11600	0.00274	similar to spermatid WD-repeat protein (LOC114987), mRNA /cds=(238,1338) /gb=NM_145241 /gi=21687047 /ug=Hs.133331 /len=3121	NM_145241	Hs.133331	NP_660284
11604	0.038855	EST(ae50c06.s1 Stratagene lung carcinoma 937218 clone IMAGE:950314 3' contains Alu repeat)	AA600135		
11606	0.006723	UI-H-DT1-avz-k-14-0-UI.s1 NCI_CGAP_DT1 cDNA clone IMAGE:5886469 3', mRNA sequence /clone=IMAGE:5886469 /clone_end=3' /gb=BQ015886 /gi=19751163 /ug=Hs.22607 /len=1207	BQ015886	Hs.22607	
11621	0.032277	ATPase, H transporting, lysosomal V0 subunit a isoform 1 (ATP6V0A1), mRNA /cds=(168,2663) /gb=NM_005177 /gi=19913417 /ug=Hs.267871 /len=4139	NM_005177	Hs.267871	NP_005168

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11629	0.024972	EST(qd99f10.x1 Soares_testis_NHT clone IMAGE:1737643 3')	AI143918		NP_005714
11671	0.004205	UI-H-DP0-avb-p-04-0-UI.s1 NCI_CGAP_Fs1 cDNA clone IMAGE:5877363 3', mRNA sequence /clone=IMAGE:5877363 /clone_end=3' /gb=BQ020727 /gi=19756005 /ug=Hs.446656 /len=1208	BQ020727	Hs.446656	
11674	0.036549	EST (qa48c04.x1 Soares_NhHMPu_S1 IMAGE:1689990 3')	AI123338		
11678	0.00299	EST (RC3-CT0369-261299-011-h06 CT0369)	AW860070		
11680	0.017843	EST ys96h09.r1 Soares retina N2b5HR cDNA clone IMAGE:222689 5'	H84275		
11684	0.013463	cDNA: FLJ21311 fis, clone COL02167. /gb=AK024964 /gi=10437390 /ug=Hs.173933 /len=3216	AK024964	Hs.173933	NP_005586
11699	0.036549	hypothetical protein MGC5306 (MGC5306), mRNA /cds=(207,1043) /gb=NM_024116 /gi=13129135 /ug=Hs.301732 /len=2336	NM_024116	Hs.301732	NP_077021
11746	0.034358	ribosomal protein L26-like 1 (RPL26L1), mRNA /cds=(43,480) /gb=NM_016093 /gi=17017971 /ug=Hs.110165 /len=723	NM_016093	Hs.110165	NP_057177
11783	0.034358	cDNA FLJ20709 fis, clone KAIA1124, highly similar to D86324 mRNA for CMP-N-acetylneuraminic acid. /gb=AK000716 /gi=7020978 /ug=Hs.24697 /len=3488	AK000716	Hs.24697	
11789	0.012525	high mobility group nucleosomal binding domain 4 (HMGN4), mRNA /cds=(239,511) /gb=NM_006353 /gi=23238232 /ug=Hs.236774 /len=1980	NM_006353	Hs.236774	NP_006344
11800	0.024972	RAN binding protein 2-like 1 (RANBP2L1), transcript variant 1, mRNA /cds=(78,5375) /gb=NM_005054 /gi=19718754 /ug=Hs.179825 /len=7164	NM_005054	Hs.179825	NP_115636
11806	0.028428	DKFZp434K0172 (from clone DKFZp434K0172) /cds=UNKNOWN /gb=AL122084 /gi=6102892 /ug=Hs.121073 /len=3447	AL122084	Hs.121073	NP_060570
11860	0.017843	FOXJ2 forkhead factor (FHX), mRNA /cds=(490,2214) /gb=NM_018416 /gi=8923841 /ug=Hs.120844 /len=4873	NM_018416	Hs.120844	NP_060886

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11879	0.049308	interleukin-1 receptor-associated kinase 4 (IRAK4), mRNA /cds=(50,1432) /gb=NM_016123 /gi=7705840 /ug=Hs.142295 /len=2817	NM_016123	Hs.142295	NP_057207
11898	0.002877	intersectin 2 (ITSN2), transcript variant 1, mRNA /cds=(242,5332) /gb=NM_006277 /gi=22325384 /ug=Hs.166184 /len=6092	NM_006277	Hs.166184	NP_671494
11923	0.002508	unidentified mRNA, partial sequence. /gb=U43604 /gi=1171236 /ug=Hs.159901 /len=1677	U43604	Hs.159901	
11926	0.043827	hypothetical protein FLJ13611 (FLJ13611), mRNA /cds=(207,1271) /gb=NM_024941 /gi=13376418 /ug=Hs.282958 /len=2726	NM_024941	Hs.282958	NP_079217
11927	0.026653	CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA /cds=(245,1123) /gb=NM_004779 /gi=24496777 /ug=Hs.26703 /len=2489	NM_004779	Hs.26703	NP_004770
11949	0.038855	spermine synthase (SMS), mRNA /cds=(102,1202) /gb=NM_004595 /gi=21264340 /ug=Hs.89718 /len=1717	NM_004595	Hs.89718	NP_004586
11955	0.041279	mRNA for KIAA0935 protein, partial cds. /cds=(1,2472) /gb=AB023152 /gi=4589513 /ug=Hs.12183 /len=6189	AB023152	Hs.12183	
11957	0.044761	DKFZp564I112 (from clone DKFZp564I112) mRNA; cDNA /cds=UNKNOWN /gb=AL110136 /gi=5817031 /ug=Hs.47679 /len=1885	AL110136	Hs.47679	
11973	0.015521	mitochondrion, complete genome	NC_001807		
11985	0.046501	protocadherin beta 16 (PCDHB16), mRNA /cds=(1156,3486) /gb=NM_020957 /gi=14195604 /ug=Hs.147674 /len=4827	NM_020957	Hs.147674	NP_066008
11987	0.030746	hypothetical protein BC008647 (LOC91875), mRNA /cds=(41,1363) /gb=NM_138376 /gi=24308431 /ug=Hs.102480 /len=1845	NM_138376	Hs.102480	NP_612385
12003	0.026653	EST(zi39c11.s1 Soares fetal liver spleen 1NFLS S1 cDNA clone 433172 3')	AA680133		NP_660208
12004	0.004569	hypothetical L1 protein (third intron of gene TS)	JU0033		JU0033
12021	0.020453	chromosome 18 open reading frame 1 (C18orf1), mRNA /cds=(243,989) /gb=NM_004338 /gi=4757883 /ug=Hs.153498 /len=8093	NM_004338	Hs.153498	NP_004329
12022	0.047541	kinesin family protein 3B (KIF3B)	NM_004798		NP_004789

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12059	0.038855	K-EST0221887 L17N670205n1 cDNA clone L17N670205n1-41-A03 5', mRNA sequence /clone=L17N670205n1-41-A03 /clone_end=5' /gb=CB161859 /gi=28147985 /ug=Hs.436333 /len=481	CB161859	Hs.436333	
12074	0.019217	EST(as88c04.x1 Barstead colon HPLRB7 clone IMAGE:2335782 3' TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN; contains Alu repeat)	AI735066		
12120	0.017843	mRNA; cDNA DKFZp761O0611 (from clone DKFZp761O0611) /gb=AL834155 /gi=21739631 /ug=Hs.22969 /len=4502	AL834155	Hs.22969	
12141	0.044761	EST (zc24f10.s1 Soares_senescent_fibroblasts_NbHSF IMAGE:323275 3')(contains Alu repetitive element)	W43004		
12155	0.011644	EST AV734861 cdA H.sapiens cDNA clone cdAAPC07 5'	AV734861		
12158	0.030134	PTK2 protein tyrosine kinase 2 (PTK2), transcript variant 1, mRNA /cds=(231,3389) /gb=NM_153831 /gi=27886591 /ug=Hs.740 /len=4453	NM_153831	Hs.740	NP_722560
12160	0.011586	DKFZp564P1871_s1 564 (synonym: hfbr2) cDNA clone DKFZp564P1871 3', mRNA sequence /clone=DKFZp564P1871 /clone_end=3' /gb=AL037446 /gi=5406837 /ug=Hs.208747 /len=556	AL037446	Hs.208747	
12163	0.016648	mRNA; cDNA DKFZp434I2129 (from clone DKFZp434I2129) /cds=(1,655) /gb=AL832450 /gi=21733015 /ug=Hs.376999 /len=2100	AL832450	Hs.376999	
12165	8.10E-04	EST CM3-HT0185-061099-021-c03 HT0185 cDNA	BE144941		
12178	0.034358	EST (of53c02.s1 NCI_CGAP_CNS1 IMAGE:1427906)	AA836671		
12183	0.004961	cDNA sequence (cDNA FLJ14256 fis, clone PLACE1000007, weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3) Length = 3176	AK024318		NP_073743
12184	0.030302	cDNA FLJ11086 fis, clone PLACE1005266. /gb=AK001948 /gi=7023529 /ug=Hs.272240 /len=1899	AK001948	Hs.272240	
12189	0.038855	EST AV750486 NPC H.sapiens cDNA clone NPCDCF06 5'	AV750486		
12207	0.004205	phytoceramidase, alkaline (PHCA), mRNA /cds=(59,862) /gb=NM_018367 /gi=19923526 /ug=Hs.23862 /len=3404	NM_018367	Hs.23862	NP_060837

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12213	0.036549	repetitive sequence (ALU SUBFAMILY J)	P39188		
12229	0.013463	clone IMAGE:3924941, mRNA /gb=BC029341 /gi=20379505 /ug=Hs.391380 /len=1657	BC029341	Hs.391380	
12243	0.021876	mRNA; cDNA DKFZp313P0434 (from clone DKFZp313P0434) /gb=AL832702 /gi=21733281 /ug=Hs.125019 /len=2995	AL832702	Hs.125019	
12244	0.00299	EST(601812732F1 NIH_MGC_54 cDNA clone IMAGE:4047222 5')	BF211120		NP_071942
12251	0.021876	AGENCOURT_10616002 NIH_MGC_141 cDNA clone IMAGE:6744199 5', mRNA sequence /clone=IMAGE:6744199 /clone_end=5' /gb=BU963194 /gi=24192766 /ug=Hs.422374 /len=939	BU963194	Hs.422374	
12252	0.015521	UI-E-CL1-afb-k-21-0-UI.s1 UI-E-CL1 cDNA clone UI-E-CL1-afb-k-21-0-UI 3', mRNA sequence /clone=UI-E-CL1-afb-k-21-0-UI /clone_end=3' /gb=BM665519 /gi=18972482 /ug=Hs.159501 /len=1100	BM665519	Hs.159501	
12259	0.026653	EST (Similar to pleckstrin homology, Sec7 and coiled/coil domains 3, clone MGC:5340 IMAGE:2984886, complete cds /cds=(3,542) /gb=BC008191 /gi=14198262 /ug=Hs.7984 /len=3720)	BC008191	Hs.7984	NP_004218
12261	0.023381	UI-E-EO1-aid-o-06-0-UI.s1 UI-E-EO1 cDNA clone UI-E-EO1-aid-o-06-0-UI 3', mRNA sequence /clone=UI-E-EO1-aid-o-06-0-UI /clone_end=3' /gb=BM677516 /gi=18987412 /ug=Hs.443680 /len=1044	BM677516	Hs.443680	
12284	0.00326	EST384170 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW971961 /gi=8161927 /ug=Hs.136340 /len=642	AW971961	Hs.136340	
12290	0.021876	EST(yd74f02.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:113979 3' similar to contains Alu repetitive element)	T79796		
12296	0.00299	EST(yy85f03.r1 Soares_multiple_sclerosis_2NbHMSP clone IMAGE:280349 5' similar to contains Alu repetitive element)	N50310		
12322	0.030302	EST(DKFZp547L234_r1 547 (synonym: hfbr1) cDNA clone DKFZp547L234 5')	AL134310		



Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12323	0.011644	hypothetical protein DKFZp564D1378 (DKFZP564D1378), mRNA /cds=(125,904) /gb=NM_032124 /gi=14149776 /ug=Hs.318401 /len=2195	NM_032124	Hs.318401	NP_115500
12326	0.036549	EST(UI-H-BI3-akh-f-06-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:2734235 3')	AW449287		
12329	0.007397	EST(RC2-CT0298-300100-014-d01 CT0298)	AW604547		NP_000981
12335	0.010816	EST (603205161F1 NIH_MGC_97 cDNA clone IMAGE:5270895 5')	BI462159		NP_006234
12352	0.036549	UI-H-BI2-ahm-d-05-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2727224 3', mRNA sequence /clone=IMAGE:2727224 /clone_end=3' /gb=AW293452 /gi=6700088 /ug=Hs.16228 /len=634	AW293452	Hs.16228	
12371	0.005259	ESTs, cDNA, 5' end /clone=BMFBFE06 /clone_end=5' /gb=AV756341 /gi=10914189 /ug=Hs.244273 /len=766	AV756341	Hs.244273	
12374	0.039601	ESTs, cDNA /gb=BG194574/gi=13716261 /ug=Hs.221776 /len=853	BG194574	Hs.221776	
12388	0.036549	EST(cDNA clone IMAGE:4398135 5')	BF984363		
12412	0.010816	cDNA / IL3-NT0294-060401-533-D04 NT0294	BI041924		
12424	0.004569	mRNA; cDNA DKFZp564B076 (from clone DKFZp564B076) /gb=AL049313 /gi=4500086 /ug=Hs.21103 /len=2208	AL049313	Hs.21103	
12426	0.036549	602590145F1 NIH_MGC_76 cDNA clone IMAGE:4724074 5', mRNA sequence /clone=IMAGE:4724074 /clone_end=5' /gb=BG564169 /gi=13571821 /ug=Hs.444093 /len=792	BG564169	Hs.444093	
12430	0.013463	mRNA; cDNA DKFZp686J19116 (from clone DKFZp686J19116) /gb=AL833458 /gi=21734100 /ug=Hs.428760 /len=3297	AL833458	Hs.428760	
12431	0.004961	ESTs, cDNA /gb=AW993259 /gi=8253410 /ug=Hs.113105 /len=678	AW993259	Hs.113105	
12433	0.041279	cDNA FLJ14388 fis, clone HEMBA1002716. /gb=AK027294 /gi=14041878 /ug=Hs.9812 /len=1673	AK027294	Hs.9812	
12435	0.028428	clone IMAGE:5263531, mRNA /gb=BC037740 /gi=22902216 /ug=Hs.18016 /len=5036	BC037740	Hs.18016	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12436	0.026653	UI-H-BW0-ajn-d-08-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2732223 3', mRNA sequence /clone=IMAGE:2732223 /clone_end=3' /gb=AW297946 /gi=6704582 /ug=Hs.444392 /len=807	AW297946	Hs.444392	
12453	0.014461	EST, cDNA, 3' end /clone=IMAGE:726989 /clone_end=3' /gb=AA398482 /gi=2051592 /ug=Hs.97641 /len=397	AA398482	Hs.97641	
12489	0.00684	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530	BF814502	Hs.446594	
12494	0.024972	cDNA FLJ39046 fis, clone NT2RP7010612. /gb=AK096365 /gi=21755841 /ug=Hs.9856 /len=2161	AK096365	Hs.9856	
12499	0.004205	EST(cDNA clone IMAGE:4823837 5' )	BG720040		NP_079229
12520	0.037211	EST(Embryonic Heart cDNA Library Danio rerio cDNA 5' )	AI617050		
12529	0.014461	cDNA FLJ36544 fis, clone TRACH2006378. /gb=AK093863 /gi=21752807 /ug=Hs.101689 /len=2670	AK093863	Hs.101689	
12530	0.024972	AGENCOURT_7566238 NIH_MGC_92 cDNA clone IMAGE:6043519 5', mRNA sequence /clone=IMAGE:6043519 /clone_end=5' /gb=BQ226831 /gi=20408231 /ug=Hs.21887 /len=1223	BQ226831	Hs.21887	
12531	0.023381	wt59c09.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2511760 3', mRNA sequence /clone=IMAGE:2511760 /clone_end=3' /gb=AI955766 /gi=5748076 /ug=Hs.329191 /len=496	AI955766	Hs.329191	
12534	0.038855	EST(cDNA clone IMAGE:1270440 3' )	AA748418		NP_060819
12555	0.016648	ESTs, cDNA, 5' end /clone=IMAGE:4802969 /clone_end=5' /gb=BG698090 /gi=13965026 /ug=Hs.12876 /len=985	BG698090	Hs.12876	
12568	0.009313	EST, cDNA, 3' end /clone=IMAGE:1541875 /clone_end=3' /gb=AA927945 /gi=3076689 /ug=Hs.292141 /len=354	AA927945	Hs.292141	
12572	0.002508	EST, clone IMAGE:4151959, mRNA /cds=UNKNOWN /gb=BC011194 /gi=15277441 /ug=Hs.367863 /len=1842	BC011194	Hs.367863	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12574	0.028428	UI-H-ED0-awx-b-15-0-UI.s1 NCI_CGAP_ED0 cDNA clone IMAGE:5824814 3', mRNA sequence /clone=IMAGE:5824814 /clone_end=3' /gb=BQ020068 /gi=19755345 /ug=Hs.396278 /len=1351	BQ020068	Hs.396278	
12593	0.047541	No significant match, ORF+2(71~409),+1(121~384)	SEQ.ID.No.94		
12618	0.030302	No significant match (ORF:+1:52~230[180])	SEQ.ID.No.28		
12624	0.021876	No significant match, ORF+3(156~314)	SEQ.ID.No.77		
12655	0.005835	zt59c06.s1 Soares_testis_NHT cDNA clone IMAGE:726634 3', mRNA sequence /clone=IMAGE:726634 /clone_end=3' /gb=AA398215 /gi=2051324 /ug=Hs.290951 /len=427	AA398215	Hs.290951	
12669	0.00632	hypothetical protein FLJ31438 (FLJ31438), mRNA /cds=(347,2107) /gb=NM_152385 /gi=22748824 /ug=Hs.24423 /len=2266	NM_152385	Hs.24423	NP_689598
12680	0.030302	EST (CM3-HT0528-010200-086-f04 HT0528)	BE169870		
12695	0.004961	mitochondrion, complete genome	NC_001807		
12697	0.005382	mitochondrion, complete genome	NC_001807		
12703	0.036549	EST(CM2-BT0366-271299-061-e10 BT0366)	BE068039		
12729	0.005835	xg60a08.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2632694 3', mRNA sequence /clone=IMAGE:2632694 /clone_end=3' /gb=AW168110 /gi=6399635 /ug=Hs.277648 /len=475	AW168110	Hs.277648	
12731	0.024972	BX099644 NCI_CGAP_Kid3 cDNA clone IMAGp998A103336, mRNA sequence /clone=IMAGp998A103336_ ; IMAGE:13 23153 /gb=BX099644 /gi=27830124 /ug=Hs.125353 /len=472	BX099644	Hs.125353	
12732	0.021876	mitochondrion, complete genome	NC_001807		
12733	0.024972	cDNA, 3' end /clone=IMAGE:2726753 /clone_end=3' /gb=AW293323 /gi=6699885 /ug=Hs.255182 /len=354	AW293323	Hs.255182	
12734	0.021876	mRNA for FLJ00201 protein. /cds=(1,2119) /gb=AK074129 /gi=18676605 /ug=Hs.353001 /len=4443	AK074129	Hs.353001	
12755	0.034358	EST(yf27d03.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:128069 3')	R09539		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12763	0.030302	UI-H-FG0-bct-g-21-0-UI.s1 NCI_CGAP_EN1_2 cDNA clone UI-H-FG0-bct-g-21-0-UI 3', mRNA sequence /clone=UI-H-FG0-bct-g-21-0-UI /clone_end=3' /gb=BU627064 /gi=23293278 /ug=Hs.85999 /len=1075	BU627064	Hs.85999	
12765	0.021876	EST (RC5-BT0663-050400-012-H04 BT0663 cDNA)	BE085097		
12779	0.032277	UI-H-DF1-auk-m-15-0-UI.s1 NCI_CGAP_DF1 cDNA clone IMAGE:5870774 3', mRNA sequence /clone=IMAGE:5870774 /clone_end=3' /gb=BM991622 /gi=19711011 /ug=Hs.24252 /len=1094	BM991622	Hs.24252	
12805	0.044761	clone IMAGE:3633225, mRNA /gb=BC012758 /gi=15706478 /ug=Hs.356377 /len=1914	BC012758	Hs.356377	
12807	0.030302	hypothetical protein BC014320 (LOC116254), mRNA /cds=(28,1020) /gb=NM_138785 /gi=20302037 /ug=Hs.240767 /len=1143	NM_138785	Hs.240767	NP_620140
12818	0.041279	7a42b09.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3221369 3', mRNA sequence /clone=IMAGE:3221369 /clone_end=3' /gb=BE551502 /gi=9793194 /ug=Hs.445382 /len=553	BE551502	Hs.445382	
12837	0.024972	cDNA, 5' end /clone=IMAGE:5214599 /clone_end=5' /gb=BI911779 /gi=16175651 /ug=Hs.121740 /len=818	BI911779	Hs.13370	NP_054763
12838	0.032277	EST(mRNA from cd34 stem cells Homo sapiens cDNA clone CBFBD10 )	AF150252		
12839	0.020453	EST383336 MAGE resequences, MAGL cDNA, mRNA sequence /gb=AW971247 /gi=8161092 /ug=Hs.348501 /len=578	AW971247	Hs.348501	
12843	0.001199	cDNA clone IMAGE:123789 3' similar to contains Alu repetitive element;contains THR repetitive element ; Soares fetal liver spleen 1NFLS	R01434		
12846	0.00684	EST, cDNA, 5' end /clone=DKFZp761D0315 /clone_end=5' /gb=AL137968 /gi=6854648 /ug=Hs.256115 /len=523	AL137968	Hs.256115	
12876	0.034358	cDNA FLJ36999 fis, clone BRACE2007518. /gb=AK094318 /gi=21753354 /ug=Hs.343588 /len=2283	AK094318	Hs.343588	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12879	0.041279	hypothetical protein FLJ22415 (FLJ22415), mRNA /cds=(342,1463) /gb=NM_024769 /gi=13376114 /ug=Hs.135121 /len=2627	NM_024769	Hs.135121	NP_079045
12888	0.003552	yp57c03.s1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:191524 3' similar to contains L1 repetitive element ;, mRNA sequence /clone=IMAGE:191524 /clone_end=3' /gb=H37807 /gi=907306 /ug=Hs.418023 /len=461	H37807	Hs.418023	
12891	0.002294	cDNA FLJ38472 fis, clone FEBRA2022148. /gb=AK095791 /gi=21755125 /ug=Hs.50150 /len=2454	AK095791	Hs.50150	
12896	0.005382	cDNA FLJ30298 fis, clone BRACE2003172. /gb=AK054860 /gi=16549479 /ug=Hs.351546 /len=2659	AK054860	Hs.351546	
12897	0.010816	EST(cDNA clone IMAGE:6106210 5')	BQ438562		NP_005339
12898	0.032277	603395193F1 NIH_MGC_90 cDNA clone IMAGE:5405278 5', mRNA sequence /clone=IMAGE:5405278 /clone_end=5' /gb=BI871283 /gi=16044958 /ug=Hs.443147 /len=845	BI871283	Hs.443147	
12903	0.00684	cDNA FLJ33097 fis, clone TRACH2000775. /gb=AK057659 /gi=16553423 /ug=Hs.415317 /len=2977	AK057659	Hs.415317	
12921	0.021876	BX106452 NCI_CGAP_Gas4 cDNA clone IMAGp998N095583, mRNA sequence /clone=IMAGp998N095583; IMAGE:2255816 /gb=BX106452 /gi=27834105 /ug=Hs.200841 /len=458	BX106452	Hs.200841	
12924	0.046501	UI-H-BI3-alm-f-10-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:2737314 3', mRNA sequence /clone=IMAGE:2737314 /clone_end=3' /gb=AW452027 /gi=6992803 /ug=Hs.440660 /len=755	AW452027	Hs.440660	
12933	0.01004	cDNA FLJ34764 fis, clone NT2NE2002311. /gb=AK092083 /gi=21750590 /ug=Hs.111583 /len=2552	AK092083	Hs.111583	
12941	0.00853	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530	BF814502	Hs.446594	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12947	0.021876	UI-H-BI1-acd-d-04-0-UI.s1 NCI_CGAP_Sub3 cDNA clone IMAGE:2713783 3', mRNA sequence /clone=IMAGE:2713783 /clone_end=3' /gb=AW135924 /gi=6140057 /ug=Hs.224883 /len=834	AW135924	Hs.224883	
12953	0.005835	cDNA, 3' end /clone=IMAGE:436024 /clone_end=3' /gb=AA699991 /gi=2702954 /ug=Hs.348162 /len=614	AA699991	Hs.348162	
12958	0.001184	ov45a11.x1 Soares_testis_NHT cDNA clone IMAGE:1640252 3', mRNA sequence /clone=IMAGE:1640252 /clone_end=3' /gb=AI073470 /gi=3400114 /ug=Hs.233388 /len=565	AI073470	Hs.233388	
12986	0.038855	mRNA; cDNA DKFZp564B222 (from clone DKFZp564B222) /gb=AL049974 /gi=4884224 /ug=Hs.100261 /len=2315	AL049974	Hs.100261	
12989	0.002294	clone IMAGE:5268470, mRNA /gb=BC040580 /gi=26251834 /ug=Hs.426563 /len=3344	BC040580	Hs.426563	
12999	0.020596	hypothetical protein FLJ32440 (FLJ32440), mRNA /cds=(228,971) /gb=NM_173685 /gi=27734760 /ug=Hs.344478 /len=1258	NM_173685	Hs.344478	NP_775956
13005	0.008631	zx55g04.r1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:446454 5', mRNA sequence /clone=IMAGE:446454 /clone_end=5' /gb=AA203502 /gi=1799213 /ug=Hs.192991 /len=952	AA203502	Hs.192991	
13014	0.041279	cDNA FLJ13334 fis, clone OVARC1001846. /gb=AK023396 /gi=10435315 /ug=Hs.269091 /len=2361	AK023396	Hs.269091	
13021	0.012483	EST(cDNA clone GLCAOE01 3')	AV646538		
13023	0.015521	UI-H-CO0-atn-a-07-0-UI.s1 NCI_CGAP_Sub9 cDNA clone IMAGE:5861653 3', mRNA sequence /clone=IMAGE:5861653 /clone_end=3' /gb=BM988193 /gi=19707582 /ug=Hs.28107 /len=1022	BM988193	Hs.28107	
13032	0.004569	EST(cDNA clone UI-R-CA0-axe-a-12-0- UI 3')	BE113844		
13033	0.011644	EST(cDNA clone IMAGE:4455676 5')	BG166249		
13053	0.023381	chromosome 3 clone RP11-627J17, WORKING DRAFT SEQUENCE, 4 unordered pieces	AC112211		
13064	0.026653	No significant match (ORF:- 1:37~186[150])	SEQ.ID.No.63		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13076	0.041279	UI-H-BI1-abw-h-07-0-UI.s1 NCI_CGAP_Sub3 cDNA clone IMAGE:2713572 3', mRNA sequence /clone=IMAGE:2713572 /clone_end=3' /gb=AW138111 /gi=6142429 /ug=Hs.436560 /len=800	AW138111	Hs.436560	
13100	0.01911	No significant match (ORF:+3:6~221[216])	SEQ.ID.No.64		
13112	0.00684	glutathione S-transferase M4 (GSTM4), transcript variant 1, mRNA /cds=(310,966) /gb=NM_000850 /gi=23065554 /ug=Hs.348387 /len=1436	NM_000850	Hs.348387	NP_671490
13128	0.038855	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA /cds=(81,362) /gb=NM_000609 /gi=10834987 /ug=Hs.237356 /len=3541	NM_000609	Hs.237356	NP_000600
13132	0.019217	endosome-associated FYVE-domain protein (ENDOFIN), mRNA /cds=(249,4868) /gb=NM_014733 /gi=7662047 /ug=Hs.83790 /len=6632	NM_014733	Hs.83790	NP_055548
13183	0.012525	translocation related non-coding gene (TNRG10) mRNA, complete sequence /gb=AF044579 /gi=3095103 /ug=Hs.375632 /len=2726	AF044579	Hs.375632	
13187	0.049308	smooth muscle cell-expressed and macrophage conditioned medium- induced protein smag-64 (LOC57086), mRNA /cds=(360,560) /gb=NM_020351 /gi=9966814 /ug=Hs.283100 /len=2828	NM_020351	Hs.283100	NP_065084
13194	0.015521	putative serine-rich protein mRNA, partial cds (AF246705.1)	AF246705	Hs.32922	NP_060102
13213	0.049308	DNA sequence from clone RP4-550H1 on chromosome 20q11.1-11.22 Contains a high mobility group protein pseudogene, a novel gene, the 5' end of the EPB41L1 gene encoding Erythrocyte membrane protein band 4.1-like 1 protein (KIAA0338), ESTs, STSs, GS>	AL035420		
13260	0.043827	UBX domain containing 2 (UBXD2), mRNA /cds=(156,1682) /gb=NM_014607 /gi=24307964 /ug=Hs.77495 /len=3867	NM_014607	Hs.77495	NP_055422
13302	6.62E-04	nuclear pore complex protein (NUP107), mRNA /cds=(116,2893) /gb=NM_020401 /gi=9966880 /ug=Hs.236204 /len=3131	NM_020401	Hs.236204	NP_065134

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13339	0.026653	mRNA for KIAA1133 protein, partial cds. /cds=(1,2676) /gb=AB051436 /gi=13195720 /ug=Hs.318584 /len=6542	AB051436	Hs.318584	
13342	0.00632	RNA guanylyltransferase and 5'-phosphatase (RNGTT), mRNA /cds=(289,2082) /gb=NM_003800 /gi=4506562 /ug=Hs.27345 /len=4546	NM_003800	Hs.27345	NP_003791
13366	0.038855	hypothetical protein DKFZp434I1916 (DKFZp434I1916), mRNA /cds=(144,563) /gb=NM_032245 /gi=14149959 /ug=Hs.334641 /len=800	NM_032245	Hs.334641	NP_115621
13376	0.023381	hypothetical protein FLJ20276 (FLJ20276), mRNA /cds=(134,3388) /gb=NM_017738 /gi=8923250 /ug=Hs.270502 /len=4790	NM_017738	Hs.270502	NP_060208
13380	0.026653	similar to HYPOTHETICAL 34.0 KDA PROTEIN ZK795.3 IN CHROMOSOME IV (MGC19606), mRNA /cds=(18,893) /gb=NM_033416 /gi=15529981 /ug=Hs.91579 /len=1074	NM_033416	Hs.91579	NP_219484
13406	0.00684	yh68a05.s1 Soares placenta Nb2HP cDNA clone IMAGE:134864 3', mRNA sequence /clone=IMAGE:134864 /clone_end=3' /gb=R32301 /gi=788144 /ug=Hs.386871 /len=246	R32301	Hs.386871	
13490	0.003866	mRNA; cDNA DKFZp586G1917 (from clone DKFZp586G1917) /gb=AL117453 /gi=5911904 /ug=Hs.306343 /len=3532	AL117453	Hs.306343	
13513	0.004961	EST(PM3-SN0020-270300-001-h08 SN0020)	AW865025		NP_115668
13515	0.030302	EST(hh87d03.x1 NCI_CGAP_GU1 clone IMAGE:2969765 3' contains Alu repeat)	AW627545		
13524	0.012525	hypothetical protein DKFZp586C1924 (DKFZp586C1924), mRNA /cds=(106,693) /gb=NM_032273 /gi=14150016 /ug=Hs.108338 /len=782	NM_032273	Hs.108338	NP_115649
13545	0.045752	yg03b02.s1 Soares infant brain 1NIB cDNA clone IMAGE:30959 3', mRNA sequence /clone=IMAGE:30959 /clone_end=3' /gb=R42618 /gi=817379 /ug=Hs.12700 /len=441	R42618	Hs.12700	
13553	0.011586	EST(zw71a05.r1 Soares_testis_NHT cDNA clone IMAGE:781616 5' similar to contains Alu repetitive element)	AA432328		
13571	0.049815	EST (7d70f02.x1 NCI_CGAP_Lu24 IMAGE:3278331 3')	BE673855		
13596	0.046501	insulin-like growth factor II receptor (IGF2R) gene, partial cds	AF069333		



Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13615	0.010816	mRNA full length insert cDNA clone EUROIMAGE 1476475 /gb=AJ420560 /gi=17066424 /ug=Hs.93231 /len=1346	AJ420560	Hs.93231	
13619	0.024441	FLJ30633 fis, clone CTONG2002418, weakly similar to Homo sapiens scaffold attachment factor B (SAF-B) mRNA (AK055195.1)	AK055195	Hs.331328	NP_079031
13634	0.023381	non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), mRNA /cds=(24,794) /gb=NM_145080 /gi=21489972 /ug=Hs.284295 /len=992	NM_145080	Hs.284295	NP_659547
13649	0.036549	Similar to heparan sulfate 6-O-sulfotransferase, clone IMAGE:3355592, mRNA, partial cds /cds=(0,518) /gb=BC001196 /gi=12654712 /ug=Hs.6363 /len=3220	BC001196	Hs.6363	NP_004798
13665	0.038855	ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA /cds=(22,459) /gb=NM_003350 /gi=12025664 /ug=Hs.79300 /len=1535	NM_003350	Hs.79300	NP_003341
13674	0.028428	mRNA for KIAA1826 protein, partial cds. /cds=(1312,2454) /gb=AB058729 /gi=14017868 /ug=Hs.266782 /len=4066	AB058729	Hs.266782	
13677	0.005835	KIAA1377 protein, partial cds /cds=UNKNOWN /gb=AB037798 /gi=7243134 /ug=Hs.188790 /len=3916	AB037798	Hs.188790	
13700	0.032277	DJ467N11.1 protein, FLJ13127 fis, clone NT2RP3002911 /cds=UNKNOWN /gb=AK023189 /gi=10435003 /ug=Hs.143917 /len=3073	AK023189	Hs.143917	NP_071374
13731	0.00274	diacylglycerol O-acyltransferase homolog 2 (mouse) (DGAT2), mRNA /cds=(777,1670) /gb=NM_032564 /gi=14211870 /ug=Hs.334305 /len=2713	NM_032564	Hs.334305	NP_115953
13746	8.95E-04	mRNA; cDNA DKFZp451N2217 (from clone DKFZp451N2217) /gb=AL832616 /gi=21733191 /ug=Hs.335812 /len=4940	AL832616	Hs.335812	
13768	0.032788	likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA /cds=(93,374) /gb=NM_014056 /gi=7661619 /ug=Hs.7917 /len=1362	NM_014056	Hs.7917	NP_054775
13784	0.046501	cDNA, 5' end /clone=UI-E-EJ0-ahh-n-05-0-UI /clone_end=5' /gb=BM716941 /gi=19030199 /ug=Hs.134353 /len=640	BM716941	Hs.134353	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13791	0.028425	hypothetical protein FLJ12787 (FLJ12787), mRNA /cds=(19,876) /gb=NM_032175 /gi=14149856 /ug=Hs.100134 /len=2751	NM_032175	Hs.100134	NP_115551
13795	0.017843	hypothetical protein FLJ21302 (FLJ21302), mRNA /cds=(91,1203) /gb=NM_022901 /gi=12597640 /ug=Hs.128071 /len=3160	NM_022901	Hs.128071	NP_075052
13814	0.036549	mRNA for KIAA0292 gene, partial cds. /cds=(1,5152) /gb=AB006630 /gi=2564331 /ug=Hs.201668 /len=6542	AB006630	Hs.201668	
13834	0.036549	hypothetical protein FLJ20186 (FLJ20186), mRNA /cds=(128,721) /gb=NM_017702 /gi=8923176 /ug=Hs.62771 /len=869	NM_017702	Hs.62771	NP_060172
13857	0.001747	mRNA full length insert cDNA clone EUROIMAGE 43432. /gb=AL109709 /gi=9187596 /ug=Hs.167456 /len=2091	AL109709	Hs.167456	
13885	0.032277	EST DKFZp434H1418_r1 434 (synonym:htes3) cDNA clone DKFZp434H1418	AL048856		NP_006531
13922	0.028428	cDNA FLJ36579 fis, clone TRACH2012647. /gb=AK093898 /gi=21752852 /ug=Hs.48653 /len=2318	AK093898	Hs.48653	
13923	0.01911	mRNA for KIAA1754 protein, partial cds. /cds=(32,1816) /gb=AB051541 /gi=12698052 /ug=Hs.28501 /len=4088	AB051541	Hs.28501	NP_203755
13945	0.007397	EST(tx88e11.x1 NCI_CGAP_Ut4 clone IMAGE:2276684 3' contains Alu repeat)	AI690725		
13952	0.046501	cDNA FLJ13342 fis, clone OVARC1001950. /gb=AK023404 /gi=10435328 /ug=Hs.255890 /len=2490	AK023404	Hs.255890	
13956	0.021876	zh79h09.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:418337 3', mRNA sequence /clone=IMAGE:418337 /clone_end=3' /gb=W92715 /gi=1421867 /ug=Hs.59358 /len=397	W92715	Hs.59358	
13959	0.030302	wi63d02.x1 NCI_CGAP_Kid12 cDNA clone IMAGE:2397987 3', mRNA sequence /clone=IMAGE:2397987 /clone_end=3' /gb=AI762877 /gi=5178544 /ug=Hs.369625 /len=467	AI762877	Hs.369625	
13982	0.007284	EST(nv54h12.r1 NCI_CGAP_Ew1 cDNA clone IMAGE:1233671)	AA721522		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13991	0.032277	cDNA FLJ35303 fis, clone PROST2009571. /gb=AK092622 /gi=21751255 /ug=Hs.131689 /len=2442	AK092622	Hs.131689	
13992	0.005942	EST oi10c01.s1 NCI_CGAP_GC4 IMAGE:1476096 3'	AA872487		NP_055862
14014	0.011644	transmembrane, prostate androgen induced RNA (TMEPAI), mRNA /cds=(321,1184) /gb=NM_020182 /gi=21361840 /ug=Hs.83883 /len=4839	NM_020182	Hs.83883	NP_064567
14033	0.026653	EST yt98a02.r1 Soares_pineal_gland_N3HPG cDNA clone IMAGE:232298 5'	H96454		
14052	0.01004	EST(tc73e11.x1 Soares_NhHMPu_S1 clone IMAGE:2070284 3')	AI379321		
14064	0.002294	hypothetical protein FLJ33918 (FLJ33918), mRNA /cds=(491,856) /gb=NM_152407 /gi=22748862 /ug=Hs.17121 /len=2811	NM_152407	Hs.17121	NP_689620
14080	0.038855	EST(af08g07.s1 Soares_testis_NHT cDNA clone IMAGE:1031100 3')	AA610081		
14093	0.034358	v-myc myelocytomatosis viral oncogene (avian) (MYC), mRNA /cds=(559,1878) /gb=NM_002467 /gi=12962934 /ug=Hs.79070 /len=2121	NM_002467	Hs.79070	NP_002458
14111	0.00632	hypothetical protein MGC3121 (MGC3121), mRNA /cds=(179,1936) /gb=NM_024031 /gi=13128979 /ug=Hs.293629 /len=2063	NM_024031	Hs.293629	NP_076936
14130	0.012525	EST (yx14d09.r1 Soares melanocyte 2NbHM IMAGE:261713 5')	N23550		
14156	0.023381	EST(nw90a09.s1 NCI_CGAP_Pr12 cDNA clone IMAGE:1253848)	AA937853		
14177	0.025245	hypothetical protein BC008207 (LOC92345), mRNA /cds=(195,1679) /gb=NM_138386 /gi=19923910 /ug=Hs.267130 /len=1919	NM_138386	Hs.267130	NP_612395
14184	0.041279	EST(clone IMAGE:2509657 3')	AI955713		
14187	0.034358	EST(RC5-HT0581-210300-021-B05 HT0581)	BE175638		
14225	0.00684	clone 23933 mRNA sequence /gb=U79273 /gi=1710239 /ug=Hs.239483 /len=1440	U79273	Hs.239483	
14226	0.014461	AGENCOURT_6480263 NIH_MGC_92 cDNA clone IMAGE:5575699 5', mRNA sequence /clone=IMAGE:5575699 /clone_end=5' /gb=BM475617 /gi=18524659 /ug=Hs.445483 /len=1135	BM475617	Hs.445483	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14235	0.041279	hypothetical protein MGC45400 (MGC45400), mRNA /cds=(245,598) /gb=NM_153333 /gi=23503246 /ug=Hs.389734 /len=1290	NM_153333	Hs.389734	NP_699164
14238	0.007994	UI-H-BI3-akh-b-10-0-UI.s1 NCI_CGAP_Sub5 cDNA clone IMAGE:2734051 3', mRNA sequence /clone=IMAGE:2734051 /clone_end=3' /gb=AW449245 /gi=6990021 /ug=Hs.438347 /len=707	AW449245	Hs.438347	
14244	0.021876	cDNA FLJ11946 fis, clone HEMBB1000709. /gb=AK022008 /gi=10433321 /ug=Hs.323231 /len=3241	AK022008	Hs.323231	
14249	0.036549	mitochondrion, complete genome	NC_001807		
14259	0.015521	BX109840 Soares_fetal_heart_NbHH19W cDNA clone IMAGp998M11793, mRNA sequence /clone=IMAGp998M11793_/_IMAGE:346930 /gb=BX109840 /gi=27877881 /ug=Hs.269512 /len=749	BX109840	Hs.269512	
14266	0.030302	EST, cDNA /clone=IMAGE:1266535 /gb=AA729300 /gi=2750659 /ug=Hs.325555 /len=173	AA729300	Hs.325555	
14268	0.036549	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA /cds=(505,1941) /gb=NM_172127 /gi=26667185 /ug=Hs.111460 /len=4098	NM_172127	Hs.111460	NP_742126
14276	0.034358	FLJ11984 fis, clone HEMBB1001348 /cds=UNKNOWN /gb=AK022046 /gi=10433365 /ug=Hs.293922 /len=3161	AK022046	Hs.293922	
14283	0.020453	ESTs, cDNA, 5' end /clone=GLCCSC04 /clone_end=5' /gb=AV720392 /gi=10817544 /ug=Hs.293568 (=ESTs, Weakly similar to AF116721 112 PRO2738)	AV720392	Hs.293568	
14295	0.012525	cDNA: FLJ22765 fis, clone KAIA1180. /gb=AK026418 /gi=10439279 /ug=Hs.163986 /len=1994	AK026418	Hs.163986	
14302	0.032277	wo01c07.x1 NCI_CGAP_Pan1 cDNA clone IMAGE:2454060 3' similar to gb:M15353 EUKARYOTIC INITIATION FACTOR 4E mRNA sequence /clone=IMAGE:2454060 /clone_end=3' /gb=AI934308 /gi=5673178 /ug=Hs.216635 /len=558	AI934308	Hs.216635	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14307	0.01004	EST(cDNA clone IMAGE:6104513 5')	BQ429184		
14322	0.015521	clone IMAGE:4297077, mRNA /gb=BC017920 /gi=17389820 /ug=Hs.375771 /len=1247	BC017920	Hs.375771	
14337	0.024972	mRNA; cDNA DKFZp686M023 (from clone DKFZp686M023) /gb=AL833547 /gi=21734192 /ug=Hs.31412 /len=7318	AL833547	Hs.31412	
14345	1.43E-04	mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624) /gb=AL110152 /gi=5817054 /ug=Hs.94030 /len=1341	AL110152	Hs.94030	
14346	0.012525	cDNA clone CBLAPH08 5'	AV739829		
14358	0.020453	nab71h02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:3273435 3' similar to contains Alu repetitive element;, mRNA sequence /clone=IMAGE:3273435 /clone_end=3' /gb=BF439932 /gi=11452449 /ug=Hs.331476 /len=347	BF439932	Hs.331476	
14368	0.032277	tu62h09.x1 NCI_CGAP_Gas4 cDNA clone IMAGE:2255681 3' similar to contains Alu repetitive element;, mRNA sequence /clone=IMAGE:2255681 /clone_end=3' /gb=AI679301 /gi=4889483 /ug=Hs.372588 /len=497	AI679301	Hs.372588	
14369	0.01911	ESTs, cDNA, 3' end /clone=IMAGE:2012069 /clone_end=3' /gb=AI357655 /gi=4109276 /ug=Hs.292931 /len=595	AI357655	Hs.292931	
14373	0.005835	UI-H-EU0-azo-e-16-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE:5851383 3', mRNA sequence /clone=IMAGE:5851383 /clone_end=3' /gb=BQ045026 /gi=19796008 /ug=Hs.446007 /len=1073	BQ045026	Hs.446007	
14374	0.001915	RC4-HT0277-160200-013-d07 HT0277 cDNA, mRNA sequence /gb=BE151126 /gi=8613847 /ug=Hs.158600 /len=571	BE151126	Hs.158600	
14379	0.043827	Similar to hypothetical protein FLJ20489, clone MGC:50559 IMAGE:5744381, mRNA, complete cds /cds=(290,1078) /gb=BC039535 /gi=24659157 /ug=Hs.440840 /len=2078	BC039535	Hs.440840	NP_776163
14384	0.015521	cDNA FLJ14041 fis, clone HEMBA1005780. /gb=AK024103 /gi=10436401 /ug=Hs.214783 /len=3488	AK024103	Hs.214783	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14386	0.038855	UI-E-EJ0-aik-i-20-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-aik-i-20-0-UI 5', mRNA sequence /clone=UI-E-EJ0-aik-i-20-0-UI /clone_end=5' /gb=BM727413 /gi=19048746 /ug=Hs.112619 /len=1667	BM727413	Hs.112619	
14390	0.01004	BX097880 NCI_CGAP_Thy1 cDNA clone IMAGp998F242841, mRNA sequence /clone=IMAGp998F242841_/_IMAGE:1133207 /gb=BX097880 /gi=27829041 /ug=Hs.208961 /len=354	BX097880	Hs.208961	
14393	0.009313	UI-CF-EN1-add-I-13-0-UI.s1 UI-CF-EN1 cDNA clone UI-CF-EN1-add-I-13-0-UI 3', mRNA sequence /clone=UI-CF-EN1-add-I-13-0-UI /clone_end=3' /gb=BM980639 /gi=19602306 /ug=Hs.363126 /len=691	BM980639	Hs.363126	
14394	0.028428	ESTs, cDNA, 3' end /clone=IMAGE:397194 /clone_end=3' /gb=AA719837 /gi=2732936 /ug=Hs.292589 /len=480	AA719837	Hs.292589	
14403	0.009313	UI-1-BB1p-avf-c-10-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-avf-c-10-0-UI 3', mRNA sequence /clone=UI-1-BB1p-avf-c-10-0-UI /clone_end=3' /gb=BQ023219 /gi=19758498 /ug=Hs.365670 /len=1038	BQ023219	Hs.365670	
14414	0.028428	AV764634 MDS cDNA clone MDSBZE01 5', mRNA sequence /clone=MDSBZE01 /clone_end=5' /gb=AV764634 /gi=10922482 /ug=Hs.270532 /len=1289	AV764634	Hs.270532	
14417	0.014461	proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), mRNA /cds=(137,922) /gb=NM_002789 /gi=23110940 /ug=Hs.251531 /len=1189	NM_002789	Hs.251531	NP_002780
14431	0.003145	cDNA clone e443-f /He443-f Adult heart, Clontech	T82627		
14444	0.005835	mitochondrion, complete genome	NC_001807		
14448	0.016648	cDNA FLJ30332 fis, clone BRACE2007254. /gb=AK054894 /gi=16549521 /ug=Hs.351572 /len=1800	AK054894	Hs.351572	
14449	0.001199	clone 25023 mRNA sequence /gb=AF131817 /gi=4406652 /ug=Hs.90858 /len=1466	AF131817	Hs.90858	
14474	0.002161	EST(cDNA clone IMAGE:4850459 3' )	BG745876		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14483	0.020453	cDNA FLJ34248 fis, clone FCBBF4000446. /gb=AK091567 /gi=21749972 /ug=Hs.112461 /len=1623	AK091567	Hs.112461	
14505	9.88E-04	No significant match (ORF:none)	SEQ.ID.No.66		
14521	0.00182	HSC15D092 normalized infant brain cDNA cDNA clone c-15d09 3', mRNA sequence /clone=c-15d09 /clone_end=3' /gb=Z39248 /gi=562440 /ug=Hs.27328 /len=352	Z39248	Hs.27328	
14524	0.004569	EST (wa75f06.x1 Soares NFL T GBC S1	AI685268		
14541	0.026229	EST tz43f04.x1 NCI_CGAP_Brn52 cDNA clone IMAGE:2291359 3' similar to contains Alu repetitive element;contains L1.b1 L1 repetitive	AI863121		
14542	0.028428	EST xn66e12.x1 NCI_CGAP_CML1 IMAGE:2699470 3' similar to contains Alu repetitive element;	AW195150		
14551	0.003434	EST (ng23f02.s1 NCI_CGAP_Ov2 cDNA clone IMAGE:930267 similar to contains Alu repetitive element)	AA502813		
14560	0.049308	TRAM-like protein (KIAA0057), mRNA /cds=(76,1188) /gb=NM_012288 /gi=6912449 /ug=Hs.153954 /len=6974	NM_012288	Hs.153954	NP_036420
14598	0.017843	cDNA FLJ32068 fis, clone OCBBF1000114. /gb=AK056630 /gi=16552085 /ug=Hs.24758 /len=2139	AK056630	Hs.24758	
14612	0.041279	EST (AL536815 LTI_FL013_FBrn1 clone CS0DF020YK05 5')	AL536815		
14613	0.047541	neuroepithelial cell transforming gene 1 (NET1), mRNA /cds=(147,1775) /gb=NM_005863 /gi=19923326 /ug=Hs.25155 /len=3236	NM_005863	Hs.25155	NP_005854
14614	0.020596	EST(yq95a02.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:203498 5' similar to contains Alu repetitive element)	H56096		
14615	0.005259	EST zb60f02.y5 Soares_fetal_lung_NbHL19W cDNA clone IMAGE:307995 5' similar to contains Alu repetitive element;contains element LTR9 repetitive element ;	AI734267		NP_079335
14633	0.034358	EST(no86d01.s1 NCI_CGAP_AA1 cDNA clone IMAGE:1113697 3')	AA614000		
14639	0.038855	EST (no81g07.s1 NCI_CGAP_AA1 IMAGE:1113276 3')	AA613881		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14643	0.028428	UI-H-FG1-bgh-l-12-0-UI.s1 NCI_CGAP_FG1 cDNA clone UI-H-FG1-bgh-l-12-0-UI 3', mRNA sequence /clone=UI-H-FG1-bgh-l-12-0-UI /clone_end=3' /gb=BU624037 /gi=23290252 /ug=Hs.416904 /len=1160	BU624037	Hs.416904	
14648	0.005713	mRNA; cDNA DKFZp667J1615 (from clone DKFZp667J1615) /gb=AL713792 /gi=19584550 /ug=Hs.120388 /len=4127	AL713792	Hs.120388	
14663	0.001747	EST(zs14a10.r1 NCI_CGAP_GCB1 cDNA clone IMAGE:685146 5')	AA243380		NP_057315
14671	0.00274	UI-H-EI0-aye-c-17-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-aye-c-17-0-UI 3', mRNA sequence /clone=UI-H-EI0-aye-c-17-0-UI /clone_end=3' /gb=CA447385 /gi=24811805 /ug=Hs.420740 /len=812	CA447385	Hs.420740	
14694	0.022058	cDNA FLJ35910 fis, clone TESTI2009987. /gb=AK093229 /gi=21752038 /ug=Hs.348902 /len=2035	AK093229	Hs.348902	
14695	0.008631	EST(cDNA clone IMAGE:1240639 3' similar to contains Alu repetitive element)	AA808945		
14697	0.020453	EST00015 NCI_CGAP_Lu5 cDNA clone IMAGE:1568018 3', mRNA sequence /clone=IMAGE:1568018 /clone_end=3' /gb=BF707422 /gi=11999083 /ug=Hs.298289 /len=858	BF707422	Hs.298289	
14698	0.011586	EST(MR1-MT0282-191200-005-b11 MT0282 cDNA )	BF904004		
14700	0.020453	EST(cDNA clone IMAGE:4761963 5' )	BG682907		NP_065750
14712	0.002621	mRNA; cDNA DKFZp564D193 (from clone DKFZp564D193) /gb=AL049252 /gi=4499993 /ug=Hs.406752 /len=3343	AL049252	Hs.406752	
14714	0.016648	UI-E-CL1-afe-n-12-0-UI.s1 UI-E-CL1 cDNA clone UI-E-CL1-afe-n-12-0-UI 3', mRNA sequence /clone=UI-E-CL1-afe-n-12-0-UI /clone_end=3' /gb=BU729525 /gi=23652495 /ug=Hs.233617 /len=1402	BU729525	Hs.233617	
14717	0.026229	cDNA FLJ32589 fis, clone SPLEN2000443. /gb=AK057151 /gi=16552741 /ug=Hs.21342 /len=2178	AK057151	Hs.21342	
14719	3.93E-04	EST(cDNA clone IMAGE:2387836 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;)	AI760555		NP_658913



Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14720	0.00684	cDNA FLJ32224 fis, clone PLACE6004336. /gb=AK056786 /gi=16552290 /ug=Hs.406907 /len=3076	AK056786	Hs.406907	
14722	0.002877	cDNA FLJ11439 fis, clone HEMBA1001299. /gb=AK021501 /gi=10432697 /ug=Hs.287416 /len=1500	AK021501	Hs.287416	
14736	0.012525	FLJ33160 fis, clone UTERU2000485 /cds=UNKNOWN /gb=AK057722 /gi=16553641 /ug=Hs.124733 /len=2328	AK057722	Hs.124733	
14737	0.034358	clone IMAGE:5298326, mRNA /gb=BC036198 /gi=23271941 /ug=Hs.369297 /len=3475	BC036198	Hs.369297	
14738	0.007397	EST(cDNA clone IMAGE:3570461 3' similar to contains element MER7 repetitive element ; )	BF115962		NP_620584
14763	0.01004	EST(cDNA clone IMAGE:2224205 3'. )	AI589443		
14769	0.007994	UI-E-EJ0-aig-I-23-0-UI.s1 UI-E-EJ0 cDNA clone UI-E-EJ0-aig-I-23-0-UI 3', mRNA sequence /clone=UI-E-EJ0-aig-I-23-0-UI /clone_end=3' /gb=BM678100 /gi=18987996 /ug=Hs.156646 /len=1091	BM678100	Hs.156646	
14773	0.002294	602635144F1 NCI_CGAP_Skn3 cDNA clone IMAGE:4780090 5', mRNA sequence /clone=IMAGE:4780090 /clone_end=5' /gb=BG741535 /gi=14052188 /ug=Hs.445822 /len=693	BG741535	Hs.445822	
14806	0.024972	cDNA FLJ14279 fis, clone PLACE1005574. /gb=AK024341 /gi=10436703 /ug=Hs.250383 /len=2005	AK024341	Hs.250383	
14819	0.030134	FLJ14036 fis, clone HEMBA1004709/cds=UNKNOWN /gb=AK024098 /gi=10436394 /ug=Hs.306663/len=2067	AK024098	Hs.306663	
14825	0.013494	clone IMAGE:3847423, mRNA /gb=BC020562 /gi=18088249 /ug=Hs.352245 /len=2742	BC020562	Hs.352245	
14831	0.023381	clone IMAGE:4183899, mRNA /cds=UNKNOWN /gb=BC008625 /gi=14250384 /ug=Hs.55336 /len=1413	BC008625	Hs.55336	
14833	0.004205	EST380251 MAGE resequences, MAGJ cDNA, mRNA sequence /gb=AW968281 /gi=8158016 /ug=Hs.319460 /len=689	AW968281	Hs.319460	

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14837	0.009313	EST(RC4-CT0322-261299-011-h03 CT0322 Homo sapiens cDNA, mRNA sequence)	AW857814		
14842	0.049308	mitochondrion, complete genome	NC_001807		
14845	0.012525	EST, cDNA /clone=IMAGE:1252723 /gb=AA888306 /gi=3003981 /ug=Hs.327126 /len=291	AA888306	Hs.327126	
14851	0.021876	UI-H-BW1-amm-h-09-0-UI.s1 NCI_CGAP_Sub7 cDNA clone IMAGE:3070696 3', mRNA sequence /clone=IMAGE:3070696 /clone_end=3' /gb=BF512783 /gi=11597962 /ug=Hs.443691 /len=568	BF512783	Hs.443691	
14877	0.028811	EST, cDNA, 3' end /clone=IMAGE:248258 /clone_end=3' /gb=N58488 /gi=1202378 /ug=Hs.94100 /len=520	N58488	Hs.94100	NP_002086
14879	0.011644	UI-H-FH1-bfm-c-24-0-UI.s1 NCI_CGAP_FH1 cDNA clone UI-H-FH1-bfm-c-24-0-UI 3', mRNA sequence /clone=UI-H-FH1-bfm-c-24-0-UI /clone_end=3' /gb=CA429379 /gi=24792105 /ug=Hs.436064 /len=1037	CA429379	Hs.436064	
14884	0.024972	602043661F1 NCI_CGAP_Brn67 cDNA clone IMAGE:4181462 5', mRNA sequence /clone=IMAGE:4181462 /clone_end=5' /gb=BF528488 /gi=11615851 /ug=Hs.433462 /len=885	BF528488	Hs.433462	
14893	0.01004	EST375707 MAGE resequences, MAGH cDNA, mRNA sequence /gb=AW963634 /gi=8153470 /ug=Hs.429581 /len=750	AW963634	Hs.429581	
14906	0.007994	EST, cDNA: FLJ21479 fis, clone COL05032 /cds=UNKNOWN /gb=AK025132 /gi=10437589 /ug=Hs.139315 /len=1920	AK025132	Hs.397727	NP_004710
14911	0.043827	UI-1-BB1p-akk-b-05-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-akk-b-05-0-UI 3', mRNA sequence /clone=UI-1-BB1p-akk-b-05-0-UI /clone_end=3' /gb=BU753775 /gi=23712051 /ug=Hs.279870 /len=1533	BU753775	Hs.279870	
14912	0.014461	cDNA FLJ25001 fis, clone CBL00443	AK057730		NP_203524
14924	0.021876	No significant match, ORF-3(1~195)	SEQ.ID.No.57		
14928	0.038855	No significant match, ORF+1(1~249),+2(11~253)	SEQ.ID.No.79		
14935	0.041279	No significant match (ORF:+1:346~452[108])	SEQ.ID.No.18		

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14942	0.007397	EST, cDNA /gb=AW360966 /gi=6865616 /ug=Hs.6653 /len=661	AW360966	Hs.6653	NP_055942
14943	0.020596	EST, mRNA; cDNA DKFZp434P0235 (from clone DKFZp434P0235) /cds=UNKNOWN /gb=AL117519 /gi=5912035 /ug=Hs.34348 /len=1124	AL117519	Hs.396951	NP_849157
14947	0.016693	EST(cDNA clone IMAGE:3267894 3' )	BF435209		
14952	0.043823	RC1-DT0029-120100-011-h01 DT0029 cDNA, mRNA sequence /gb=AW579207 /gi=7254256 /ug=Hs.414692 /len=697	AW579207	Hs.414692	
14971	0.008631	No significant match (ORF:+3: 3~180[179])	SEQ.ID.No.20		